

APPENDIX 21. AN ANALYSIS OF THE HABITAT CAPABILITY OF THE BITTERROOT ECOSYSTEM FOR GRIZZLY BEARS

Public comment received on the Draft Environmental Impact Statement for Grizzly Bear Recovery in the Bitterroot Ecosystem indicated substantial concern about the amount and quality of habitat included in the Bitterroot area and the contribution of a restored grizzly bear population in the Bitterroot to the recovery and continued existence of grizzly bears south of Canada. Some commentors indicated that they thought that the designated recovery area was too small and did not provide sufficient habitat for the needs of a recovered population of bears. Other comments questioned the number of bears that could be supported by habitat within the wilderness and multiple use lands identified in the alternatives.

A special appropriation was made by Congress for the U.S. Fish and Wildlife Service to study these issues more thoroughly in the Final Environmental Impact Statement. The four reports in this appendix apply the best available scientific approaches to answer these questions. Three reports were produced by Dr. Mark Boyce using this funding. The fourth report was produced by the Craighead Wildlife-Wildlands Institute and is included here because the information is pertinent to the question of habitat capability of the Bitterroot Ecosystem for grizzly bears.

The first report, **Relating Populations to Habitats using Resource Selection Functions** (Appendix 21A), details a methodology to relate habitat to population size utilizing grizzly bears as an example. This methodology was specifically developed for this Bitterroot project and it has subsequently been accepted for publication in a peer reviewed scientific journal.

The second report, **The Application of Resource Selection Function Analysis to Estimate the Number of Grizzly Bears that Could be Supported by Habitats in the Bitterroot Ecosystem** (Appendix 21B), applies the methodology developed in the first report to the Frank Church and Selway-Bitterroot Wilderness, and non-wilderness public lands to the north (North Fork of the Clearwater River drainage) in order to estimate the number of grizzly bears that can be expected to be supported by the habitat in these areas.

The third report, **Metapopulation Analysis for the Bitterroot Grizzly Bear Population** (Appendix 21C), describes the changes in the probability of existence of grizzly bears south of Canada with and without a restored Bitterroot population.

The fourth report, **Excerpts from and Synopsis of Portions of the Report, “Abundance and Spatial Distribution of Grizzly Plant-Food Groups in the Salmon-Selway Ecosystem: A Preliminary Analysis and Report” (Hogg, Weaver, Craighead et al. 1999)** (Appendix 21D), presents detailed habitat maps showing the distribution and abundance of major grizzly bear foods in the Bitterroot Ecosystem in east-central Idaho.

Together, these reports present significant new information on the capability of the Bitterroot Ecosystem to support grizzly bears, the distribution and abundance of the foods grizzly bears would use in this area, and the level of improvement that would occur in grizzly survival south of Canada if grizzly bears were restored in the Bitterroot Ecosystem.

APPENDIX 21A. DESCRIPTION OF METHODOLOGY UTILIZED FOR BITTERROOT POPULATION ANALYSIS PRESENTED IN APPENDIX 21B

(Note: This paper has been accepted for publication in the journal, *Trends in Ecology and Evolution*.)

Relating Populations to Habitats using Resource Selection Functions

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Habitat use can be characterized by resource selection functions (RSFs) that are proportional to the probability of an area being used by an animal. We highlight two procedures that recently have been used to relate RSFs to population density, dependent upon which field procedures are practical for a species. These new developments allow RSF models to be interfaced with geographical information systems (GIS) to map the probability of use, and ultimately populations, across landscapes.

‘Ecology is the scientific study of the distribution and abundance of organisms.’¹ If we know the distribution of resources on which the organisms depend, the distribution and abundance of organisms often can be characterized by resource selection functions (RSF). As such RSFs are fundamental tools for the quantification of ecology. An RSF is any function that is proportional to the probability of use of a resource unit². The recent development of RSFs is an offshoot of quantitative models for characterizing natural selection³, involving the use of the same statistical approaches for quantifying selection of resources by animals². The purpose of this review is to chronicle new advances in the use of RSFs for mapping the abundance of organisms using geographical information systems (GIS) and for estimating total population size in an area.

Habitat selection is usually a behavioural consequence of animals actively selecting where they live, or passively persisting in certain habitats. Ultimately, however, resource-use patterns are a consequence of the influence of selection on survival and reproduction that determines fitness in various habitats⁴. Typically, the extent of habitat use suggests the quality and abundance of resources in those areas, which in turn reflects fitness in that habitat⁵, although there are exceptions⁶.

Recent developments in the use and analysis of geographical information systems (GIS) provide the opportunity to map habitats^{7,8}. We believe that RSFs are the most promising of procedures proposed for study of resource selection when combined with GIS because: (1) RSFs offer a quantitative characterization of resource use; (2) RSFs can accommodate virtually any type of resource being selected including both categorical and scalar variables²; and (3) RSF models easily accommodate spatial structure^{9,10} and can be interfaced with GIS to facilitate rapid analysis and use of remote sensing and other types of spatial data^{8,11}.

Because RSFs yield probabilities proportional to use, we will explain how RSFs also can be used, with appropriate scaling, to tie populations to their habitats. If such a habitat/population link can be established, there are important applications for conservation and ecological management. For example, the RSF approach has been used to model populations of spotted owls (*Strix occidentalis caurina*) in the Pacific Northwest¹², to anticipate future timber wolf (*Canis lupus*) populations in the Northern Great Lakes states¹³ and New England¹⁴, to base a population viability analysis of California gnatcatchers (*Poliophtila c.*

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californica)¹⁵, and we are currently using RSFs to anticipate the distribution and abundance of grizzly bears (*Ursus arctos horribilis*) in the proposed recovery zone in the Selway-Bitterroot wilderness of Idaho and Montana (M.S. Boyce, *et al.*, unpublished).

We will outline two approaches that have appeared for linking RSFs to population size, N . Using a reference area of known N , RSFs can be used to extrapolate N in a new area based on the area of resource units. RSFs are typically estimated using use vs. availability data. Alternatively, a resource selection probability function (RSPF) can be estimated over a finite collection of sample units, which simply can be summed over an area to estimate population size. RSPFs can be obtained from samples of used vs. unused resource units or by adjusting an RSF based on sampling intensity.

Using resource selection functions

The beauty of RSFs is that they are proportional to the probability of use of a resource unit² (Box 1).

BOX 1. Estimating resource selection functions (RSFs)

A variety of statistical approaches can be used to estimate an RSF, w_i , most simply as the proportion of used resource units of category i from those available. If a_+ is the population of available resource units and a_i are those in category i , we can estimate a simple selection ratio:

$$w_i = o_i / a_i$$

where $a_i = a_i / a_+$, and similarly, o_i is the proportion of used resource units in category i . This ‘foraging ratio’ was first applied by R. E. Savage in 1931 to herring feeding on plankton off the coast of England¹⁶.

We can carry this idea a step further by modelling the use of habitats relative to their availability. For example, we might assume that our resource selection function, $w(\mathbf{x})$, can be characterized by a log-linear model:

$$w(\mathbf{x}) = \exp(\beta_0 + \beta_1 x_1 + \beta_2 x_2 + \dots + \beta_k x_k)$$

where the x_i denote $i = 1, \dots, k$ independent habitat variables, and the β_i s are selection coefficients. This model can be fitted using a generalized linear model assuming Poisson counts for the number of used units², but a short-cut is to fit a logistic model, $\phi(\mathbf{x})$, to the independent variables where the dependent data are 1 for used units and 0 for available units,

$$\phi(\mathbf{x}) = \frac{\exp(\beta_0 + \beta_1 x_1 + \beta_2 x_2 + \dots + \beta_k x_k)}{[1 + \exp(\beta_0 + \beta_1 x_1 + \beta_2 x_2 + \dots + \beta_k x_k)]}.$$

The selection coefficients, β_i , in the log-linear model are estimated by the logistic regression coefficients. We simply use the numerator, $w(\mathbf{x})$, to distribute the use of resources across the landscape².

As such, if we know the distribution of a population among habitats by RSF values in a baseline area, we can estimate the density of animals by habitat type, under the assumption that all units are equally available. If similar use patterns can be assumed to occur in another area, we can predict the population by applying densities by habitats (Box 2).

BOX 2. Estimating population size using RSFs

For the i th habitat type with area $A(x_i)$ and habitat vector x_i the relative use is:

$$U(x_i) = w(x_i)A(x_i) / \sum_j w(x_j)A(x_j)$$

where the summation is over the number of habitat types, $j = 1, 2, \dots, m$. If every habitat unit has a unique value of the variables x_i then the sum is over the number of units in the study area. So, the number of animals expected in the i th habitat type is:

$$N_i = N(U(x_i))$$

and density of animals, $D(x_i)$, in the i th habitat type is obtained by multiplying the total population size, N , by the relative use adjusted by area:

$$D(x_i) = N U(x_i) / A(x_i).$$

When applied to a new area, to estimate the population size, we simply sum over the product of density times area of the j th type of habitat in the new area, $A(x_j)$ for $j = 1, 2, \dots, m$:

$$N = \sum_j D(x_j)A(x_j)$$

Standard errors for N , and $D(x_j)$ can be approximated by the delta method using the first few terms of a Taylor series expansion¹⁷.

We provide an example using this method for extrapolating the number of wolves in the northeastern United States (Box 3). The example in Box 3 arbitrarily defines suitable habitats as those with relative RSF > 0.5, but there is no reason to expect that poorer quality habitats would not be occupied as well, thereby the calculations yield underestimates of expected population size (also see refs. 15 & 22). An extensive statistical treatment of RSFs and their estimation under various sampling protocols is provided by Manly *et al.*² and related sampling considerations are discussed by Aebischer *et al.*²³.

Using resource selection probability functions

Whereas an RSF permits us to calculate w , which is proportional to the probability of use for a resource unit, a resource selection probability function (RSPF) is scaled so that we can calculate w^* , which is the actual probability of use. Obtaining probabilities of use is useful because we simply can sum the probabilities of use over an area to estimate total population size. A study design suited to estimation of RSPFs is based on characterizing used and/or unused sample units (Box 4). However, a common problem with the used and/or unused sampling scheme is that often we cannot discern what constitutes an unused habitat unit²⁴. If we wait longer or collect data more intensively, we may discover that a habitat unit is used making the distinction between used and unused less clear. A solution to this problem is to estimate an RSF

BOX 3. Wolves in northeastern United States.

Mladenoff et al. projected wolf populations for the Great Lakes states⁹ and New England¹⁰ using resource selection functions (RSFs) with a variation on the procedure that we outlined in Box 2. They monitored wolf packs using radiotelemetry¹⁸ to secure a collection of 14 'used' pack areas containing at least 50 telemetry locations. Within the region of potential but unused habitat, they obtained habitat data from a collection of 14 random areas equal in area to the mean pack size. Each selected area was at least 10 km from the nearest known wolf pack. Therefore, the data were from used and unused sites, appropriate for a direct application of logistic regression analysis² (see Box 4). Habitat variables included road density, prey (white-tailed deer [*Odocoileus virginianus*]) density, land cover type, human population density and land ownership. Road density (R) was the best predictor. The results of the logistic regression can be expressed as a logit function. The RSF is therefore:

$$\text{logit}(p) = 14.6R - 6.6$$

The resulting logistic-regression model was scaled from 0 to 1 (i.e., a relative RSF). Suitable habitat was mapped using GIS based on areas with a relative RSF value of 0.5 or greater.

Using these suitable habitat areas, Mladenoff et al. employed two methods to extrapolate the eventual wolf population into Wisconsin and Michigan where wolf populations had recently become established. These methods were based on: (1) mean territory size, and (2) white-tailed deer (*Odocoileus virginianus*) density for prey. In the first case, the number of wolves was predicted using Fuller *et al.*'s¹⁹ model:

$$N = [AW/[M(1 + i)]]/(1 - d)$$

where N is the number of wolves, A is the area of favorable habitat, W is the mean pack size (4.08), M is the mean pack territory size (179 km²), i is the proportion of saturated habitat in interstitial areas between packs (0.37), and d is an estimate of the proportion of non-pack wolves (0.15). Isolated habitat fragments less than 50 km² were not included. This method, therefore, offers an estimate of the saturated wolf density at equilibrium given pack characteristics such as those observed in Minnesota.

The second method extrapolates wolf population density, D in numbers per 1,000 km², based on a prey density estimate, specifically white-tailed deer density per km², X :

$$D = 3.4 + 3.7X$$

where deer density was estimated for each deer management unit by state wildlife officials^{20,21}. Again only 'suitable' habitat was used for the extrapolation and habitat fragments less than 50 km² were deleted. An illustration of anticipated wolf habitats in New England is presented in Figure 6-8 (a) where prey includes both deer and moose (*Alces alces*). Wolf population size was obtained simply by summing over the areas of interest Figure 6-8 (b).

By monitoring the expanding wolf population in northern Wisconsin subsequent to publishing their model, Mladenoff et al. validated the model²¹ although finding that wolves will indeed occupy areas with RSF < 0.5.

using a generalized linear model assuming Poisson counts for the number of used units². A short-cut (Box 1) is to fit a logistic regression of used versus available sites, and then to adjust the RSF for different sampling intensities of randomly selected units (available) and used units².

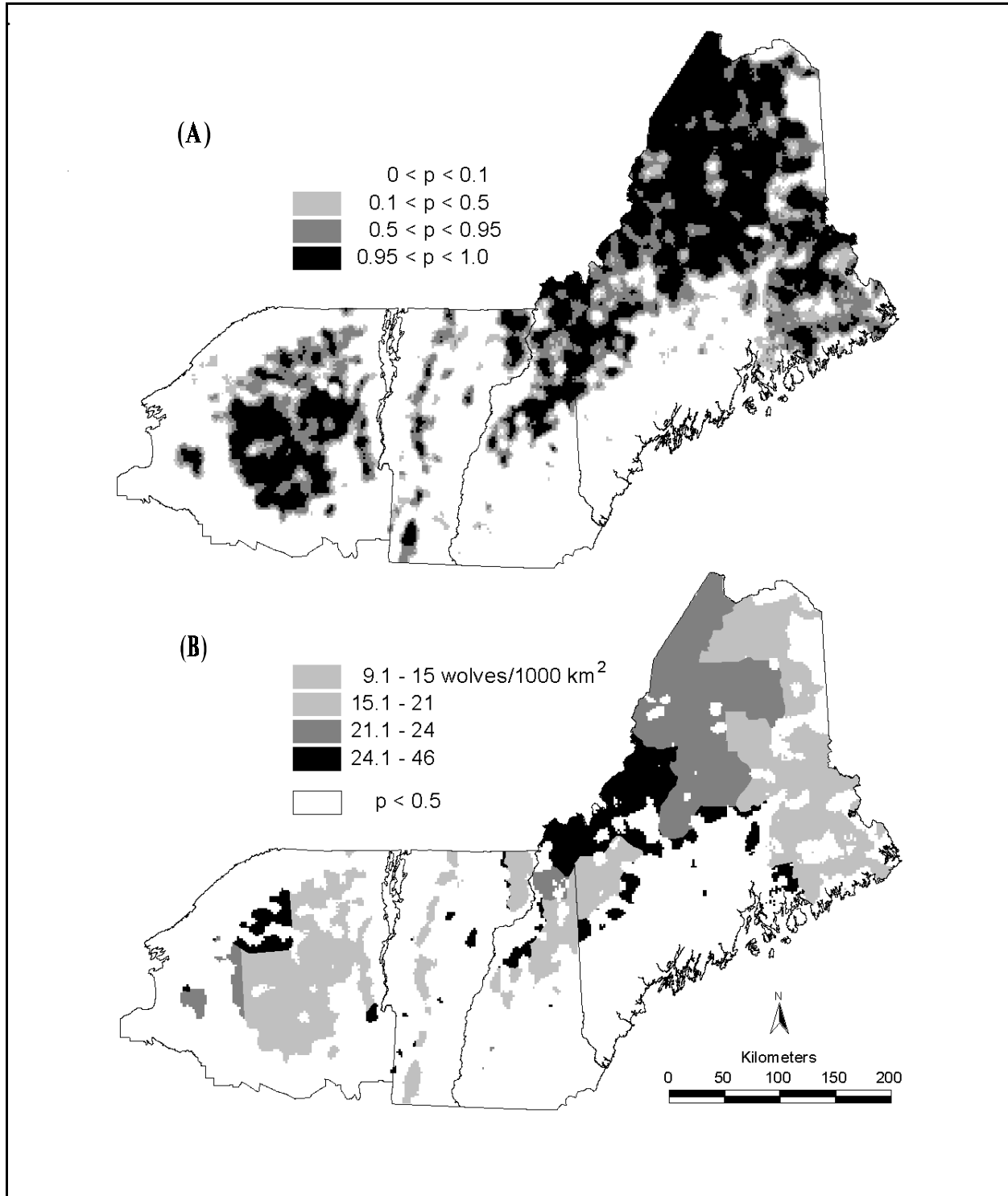


Figure 6-8. Potential wolf habitats in New England classified according to relative RSF scores, where classes with $p > 0.5$ were classified as favorable habitat (a). Potential wolf densities (b) were based on a combination of favorable habitat from map (a) and prey abundance. Modified, with permission, from Ref. 14.

BOX 4. Estimating resource selection probability functions (RSPFs)

There are several study designs that can yield an RSPF directly. Perhaps the easiest approach for estimating an RSPF, $w^*(\mathbf{x})$, is to use logistic regression on samples of used and unused units, where the selection function is modeled by a logistic function of k independent variables, x_i , hypothesized to influence resource selection and β_i are coefficients to be determined when fitting the model to data:

$$w^*(\mathbf{x}) = \exp(\beta_0 + \beta_1 x_1 + \beta_2 x_2 + \dots + \beta_k x_k) / [1 + \exp(\beta_0 + \beta_1 x_1 + \beta_2 x_2 + \dots + \beta_k x_k)]^{2,24}.$$

Many statistical packages are available for logistic regression. Input data are the dependent variable (either 0 for unused units or 1 for used units) and the corresponding values of the independent variables, x_i , measured on each unit. This approach yields outcomes directly interpretable as probabilities or alternatively as a ratio of odds.

Thus, for a finite number of possible habitat units, we first measure resources for a sample of used and available sites. Then we use logistic regression to estimate an RSF to characterize habitat use patterns. The RSF equation is then modified to create an RSPF by altering the constant, β_0 , to adjust for differential sampling of random habitat units and used sites². The RSPF model then can be applied to a GIS map, predicting population size by summing the RSPF probabilities over an area of interest.

With this method, RSPFs are computed from samples of resource units that are finite in number. If the sampling unit is a point, say a radiotelemetry location, scaling logistic regression for RSPF is not possible because there are an infinite number of possible sampling units. Estimating population size using RSPFs is most easily adapted to territorial species where individuals (or families) occupy exclusive areas (Box 5). When territories overlap, however, an RSPF still could be used to estimate population size by adjusting for the extent of territory overlap.

Assumptions of RSF-based population estimation

We assume that the modeler knows the limiting factors that influence the distribution and abundance of the study organism and that data are available on key resource variables. When resource units are sampled, we also assume that these are sampled randomly and independently. We further assume that organisms have free and ready access to available resource units. Although we assume that RSFs and resources do not change during the study, this assumption can be relaxed if sufficient data are available to estimate RSFs repeatedly. In some applications, habitats are dynamic and change rapidly, but RSFs can be estimated to document how resource selection changes through time. For example, Arthur et al.¹¹ studied variation in pack ice as habitat for polar bears (*Ursus maritimus*) and measured habitat selection every three to six days. Similarly, seasonal changes in habitat use may require one to estimate RSFs by season²⁷.

In addition to the issue of temporal constancy in resource selection, we also must struggle with variation in the availability of resources and the effect of spatial variation on selection of a given unit. If not reconciled, an RSF or RSPF estimated in one area cannot be applied in another area except under some unusual circumstance where the availabilities, including effects of spatial variation, are the same. Indeed, simply varying the size of the study area or excluding certain areas from the domain of the study can result in different models²³. This is not a fatal flaw, however, because sometimes we obtain robust models that are

BOX 5. Northern spotted owls in the Pacific Northwest

Declines in habitat for the northern spotted owl (*Strix occidentalis caurina*) in the Pacific Northwest have been a major conservation concern during the past decade. We used RSF to evaluate the role of habitat variables in the distribution of spotted owl nest sites, including several measures of landscape pattern such as patchiness, isolation, contagion and fractal dimension²⁶. Our sample unit was a 2-km² circle surrounding an owl site, approximately the area of an exclusively defended territory for a pair of owls. An intensive field survey effort by U.S. Bureau of Land Management (BLM) and Forest Service personnel censused a total of 1 780 owl pairs within the bounds of our study area in western Oregon (USA). We measured details of habitat within 2-km² circles at 50 owl sites and 50 random forest-landscape locations.

We used logistic regression to estimate an RSF from a set of habitat variables that we hypothesized to be important to the owls viz:

$$w^* = \exp[\beta_0 + \beta_1(OldGrowth) + \beta_2(ElevRange) + \beta_3(Diversity)]$$

where *OldGrowth* is the area within the 2-km² circle in old-growth forest, *ElevRange* is the range in elevation at the site, and *Diversity* is the Shannon Index of the diversity of forest types within the 2-km² circle.

Key to linking this relative RSF to population is the calculation of β_0 . Following Manly *et al.*² we estimated the β_0 from the logistic regression analysis by subtracting the ratio of sampling fractions, P_u/P_a . Here P_u is the proportion of used units sampled and P_a is the proportion of available units sampled. Assuming that the BLM/Forest Service census of 1,780 spotted owl pairs up to 1993 was valid, $P_u = 50/1,780 = 0.028$ because we measured habitats for 50 out of 1,780 possible pairs of owls. Likewise, we measured habitats at 50 nonoverlapping random landscape locations out of 18,079 possible 2-km² plots that would cover the entire study area yielding $P_a = 50/18,079 = 0.0028$. Thus, a total of 1 780 owls occupied a total available 18,079 sites or 9.8% of the sites were used¹².

We then estimated w^* s for each of 50 landscape locations obtaining a mean w^* of 0.098 (± 0.031 95% C.I.), which is virtually identical with the proportion of available 2-km² plots used by spotted owls. The locations of these owls were accumulated over more than 10 years of sampling, and a substantial number of the sites had been monitored for several years. Our estimate of w^* is to characterize the location of owl sites, but these owl sites vary in how frequently they were occupied. We estimated the proportion of years that each site was occupied, and again modeled this as a function of habitat variables but using linear regression. Then this proportion was multiplied by w^* , which yielded the probability that a 2-km² area is an occupied owl site. By summing these over the study area, we estimated the total population size, thereby allowing our calculations to be cross checked¹².

relatively insensitive to variation in availabilities, and in other cases we can model the relation between selection coefficients and availabilities explicitly, thereby taking availabilities into account.

When certain habitat attributes are key to the ecology of a species, the coefficients can be robust over a range of habitat types. This was the case for spotted owl models because old growth was such an overwhelmingly important variable in our estimation of RSFs—the amount of old growth forest was a good predictor even in quite different landscapes²⁶. Specifically, the RSF estimated for habitats in southwestern Oregon accurately predicted spotted owl locations on the Olympic Peninsula and on the east slope of the Cascades of Washington—both of these areas host very different vegetation. However, because the amount of old growth forest was such an overwhelmingly important ecological variable, it was a strong predictor in each area and the models could be used interchangeably among areas with little loss of accuracy in predicting

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owl nest sites (Box 5).

In some circumstances, resource availabilities in a landscape vary considerably, as do the diets of animals in different habitats. Consider, for example, grizzly bears in the Yellowstone (USA) ecosystem. Some bears have seasonal access to cutthroat trout (*Oncorhynchus clarki*), whereas other bears may have no trout streams within their home ranges²⁸. Likewise, some bears feed extensively on army cutworm moths (*Euxoa auxiliaris*) in alpine talus, but, again, some bears have no access to this food resource²⁹. Availability of certain resources influences diet and habitat-use patterns. One solution to this problem is to sample home ranges over a range of habitats, and then to model the coefficients in the RSF as a function of the availability of resources in each home range. Modelling the coefficients might be accomplished using linear regression analysis, for example. Then when a new area is modeled, the β_i coefficients will be estimated based on the availabilities in this new area.

One of the potential applications of RSF models in GIS context is to project future habitats using succession models, and then to anticipate future population sizes¹². Understanding how RSF coefficients might change as resource availabilities change on the landscape is fundamental to the reliability of such population projections.

Autocorrelation of resource variables is an important consideration, especially for evaluating the statistical significance of alternative models. Autocorrelated data tend to yield estimates of variance that are too small and consequently we are likely to overestimate the differences of use among habitats². Radiotelemetry data, for example, might be abundant but not independent. By inspecting an autocorrelation function, one can identify the time interval over which observations become independent and use this interval for sampling observations.

Likewise, the distribution of organisms is seldom random in space, and we often find them to be clustered in good habitat or possibly aggregated as an antipredator strategy. But the spatial autocorrelation structure of the distribution of the organism might be simply a function of the spatial pattern of its habitats, so RSF modelling might remove any such pattern. One approach is to examine the residuals from an RSF to see if spatial aggregations occur independently of habitat; for example by using the Durbin-Watson statistic. If spatial autocorrelation occurs in the residuals, as a next step one might develop autologistic models where the animals' use of resource units surrounding a used resource unit is a covariate in a logistic regression model⁹. Alternatively, one might use an interpolation method like kriging³⁰ or some other smoothing algorithm to create 'nicer' maps of distribution. For purposes of projecting population size, however, the β_i -coefficients in a logistic regression model are not biased by spatial autocorrelation, so estimates of population size should not be affected. The primary advantage of modelling the spatial autocovariance is to create more realistic maps of distribution.

Implicit in attempts to model populations based on habitats is an assumption of equilibrium population dynamics. If populations are changing rapidly, we cannot expect RSF models to hold constant. Two possible approaches to this problem come to mind. First, one might model RSFs at varying population densities to see how the coefficients vary in a density-dependent fashion³¹. Another approach would be to model mean population densities assuming that population fluctuations are attributable to stochastic fluctuations around some long-term average¹². Otherwise, applications will be limited to species with equilibrium dynamics occurring at or near carrying capacity.

The value of habitats is not necessarily based upon their use⁶. For example, habitats used for sleeping might not be in short supply nor all that crucial for survival. Access to water, however, might be crucial but only a few minutes each day might be spent drinking. Other approaches can be taken to evaluate the importance of habitats. For example, one might multiply the RSF values by the caloric food value of each habitat to get an index of the value of a habitat (D.J. Mattson, unpublished). Another approach is to model

the reproduction or survival of individuals as a function of habitat variables thereby dissecting components of fitness. An understanding of the ecology of the species must be used in the interpretation of RSF models.

Research opportunities

Summarizing his review of definitions of ecology, Krebs³² suggested that ‘We are interested in *where* organisms are found, *how many* occur there, and *why*’. RSFs can do an excellent job of describing where, and under certain assumptions, how many. But RSFs are simply statistical descriptions of the distribution and use of landscapes, and as such, do not necessarily help us to understand why organisms are where they are. In contrast to individual-based models³³ that typically include many details, RSFs take a broad-scale or top-down perspective characterizing general patterns on the landscape. RSFs generally will be preferable to individual-based models when data are scarce and the spatial scale is large. When applicable, RSFs offer a framework from which one can explore the ecological processes that shape distribution and abundance.

Habitat ecology is a discipline depauperate of theory, even though habitats are fundamental to population biology, community ecology, behavioural ecology, landscape ecology, conservation biology and wildlife management. Indeed, given the definition of ecology at the beginning of this article, one might argue that habitat ecology rests at the very core of ecology.

There are several reasons for the lack of a theory of habitat ecology. By its very nature, habitat ecology is a multifaceted process requiring simultaneous consideration of a number of variables. However, RSF based on multivariable models such as multiple logistic regression easily accommodates this problem. Interactions with other species, influences of a variety of physical and biotic factors, and the structure of the population can all be built into the model explicitly. Furthermore, habitat ecology is fundamentally in a spatial context which has always been difficult to model. Issues of scale are readily explored using RSFs constructed at alternative scales²⁷, or even multiple scales²⁶. Recent advances in GIS technology make spatial modelling much easier, especially when facilitated by RSFs.

RSFs can provide a framework for the development of a theory of habitat ecology. The simple methods that we have outlined in this paper forge a link between landscape ecology and population biology. More generally, however, ecological and behavioural processes shape the RSF coefficients. Foraging theory is behind the prediction of resource selection, providing the mechanisms that shape patterns of resource use. Likewise, physiological ecology is fundamental to predicting resource needs of organisms. If we can build models to predict the ρ_s , we can generalize models that incorporate the processes.

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APPENDIX 21B. THE APPLICATION OF RESOURCE SELECTION FUNCTIONS ANALYSIS TO ESTIMATE THE NUMBER OF GRIZZLY BEARS THAT COULD BE SUPPORTED BY HABITATS IN THE BITTERROOT ECOSYSTEM

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A resource selection function (RSF) is any function that is proportional to the probability of use of a resource unit (Manly et al. 1993). If resource units are selected carefully, they can characterize habitat for a species. Given a reference area of known density of animals, one can estimate potential population size based on habitat RSFs derived for the study area and the reference baseline area (Boyce and McDonald 1999). We use this approach to estimate the potential number of grizzly bears (*Ursus arctos horribilis*) in the proposed recovery area in the Selway-Bitterroot wilderness of Idaho and Montana (USFWS 1997).

METHODS

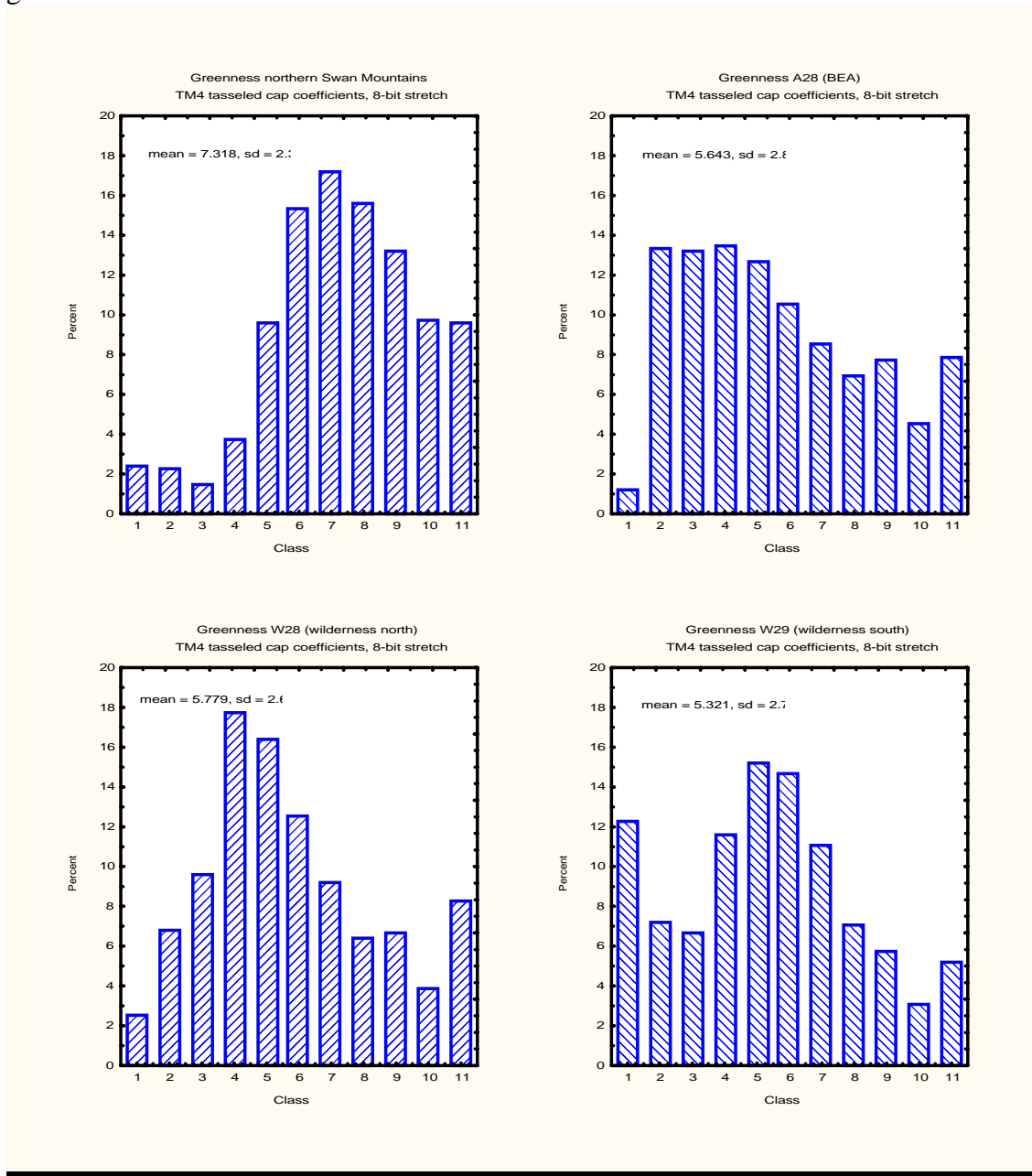
A north to south gradient in precipitation occurs in the Bitterroot recovery area such that the northern half of the area is much wetter with denser vegetation than the southern half. Because of this gradient, we developed estimates of the number of bears using two baseline populations: (1) the northern Swan Mountains study area which is wetter than (2) the Yellowstone ecosystem. We developed population estimates for the southern half of the Bitterroots using an RSF from the Yellowstone ecosystem, and both the north and south halves of the Bitterroots using the northern Swan Mountains model. The histograms presented in Figures 6-9 through 6-14 compare the areal percentage of each model parameter in the reference and extrapolation areas. By calculating estimates for the southern half using both sets of models we can compare results using the two reference areas although we believe that the Yellowstone ecosystem is a better ecological baseline for comparison with the southern half of the Bitterroots.

Bitterroot Habitat Model

To build an equation that predicts relative probability of use of habitats in the Selway – Bitterroot, we used an existing grizzly bear radio-telemetry database. This telemetry data was collected during 1988-1994 by the Montana Department of Fish, Wildlife and Parks in the northern Swan Mountains during the South Fork Grizzly Project. We believed that the northern Swan Mountains were sufficiently similar to the northern Selway – Bitterroot to allow extrapolation of general grizzly bear habitat relationships. The northern half of the Selway - Bitterroot was divided into two regions: the core wilderness area, and the non-wilderness portion of the Bitterroot Evaluation Area (BEA) to the north (Davis and Butterfield 1991). The model was also extrapolated to the southern Selway – Bitterroot as a comparison to values derived from the Yellowstone Ecosystem model. We compared the availability of various digital data layers between the northern Swan Mountains and the Selway – Bitterroot wilderness. We selected 7 layers that were good predictors of grizzly bear habitat use and that could be replicated between each study area. The layers were:

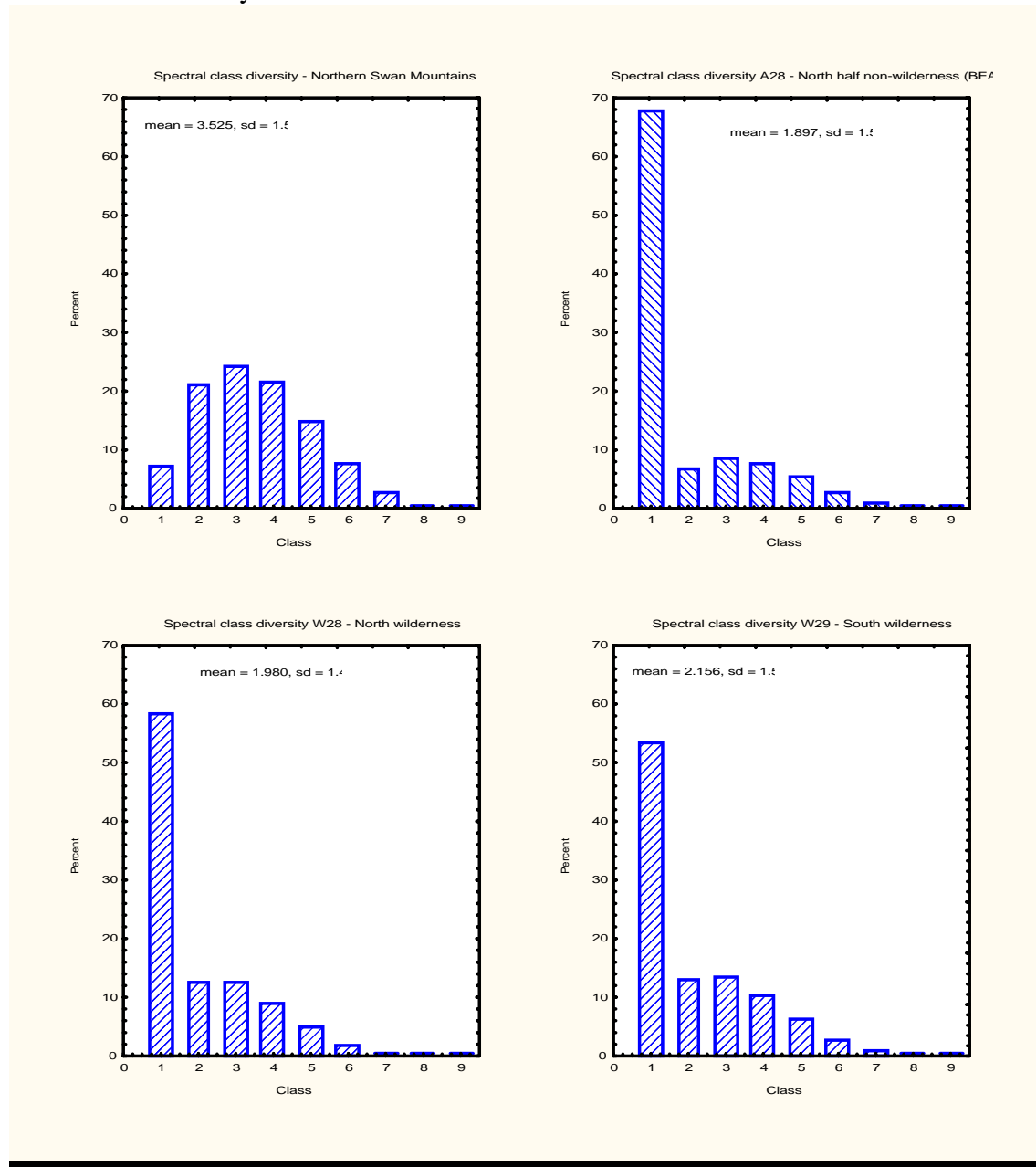
Greenness – a measure of vegetation reflectance derived from Thematic-Mapper satellite imagery, analogous to leaf area index. The imagery used in the South Fork Flathead is described in Mace et al. 1997. To produce the Selway – Bitterroot greenness layer, we did a tasseled cap transformation on TM scene p41r28 (20 July, 1991) and p41r29 (31 July, 1995) as described in Manley et al. (1992) and Mace et al. (1997).

Figure 2. Greenness in the northern Swan Mountains reference area and each of the 3 extrapolation regions. The ordinate axis refers to the percent of area within each greenness class.



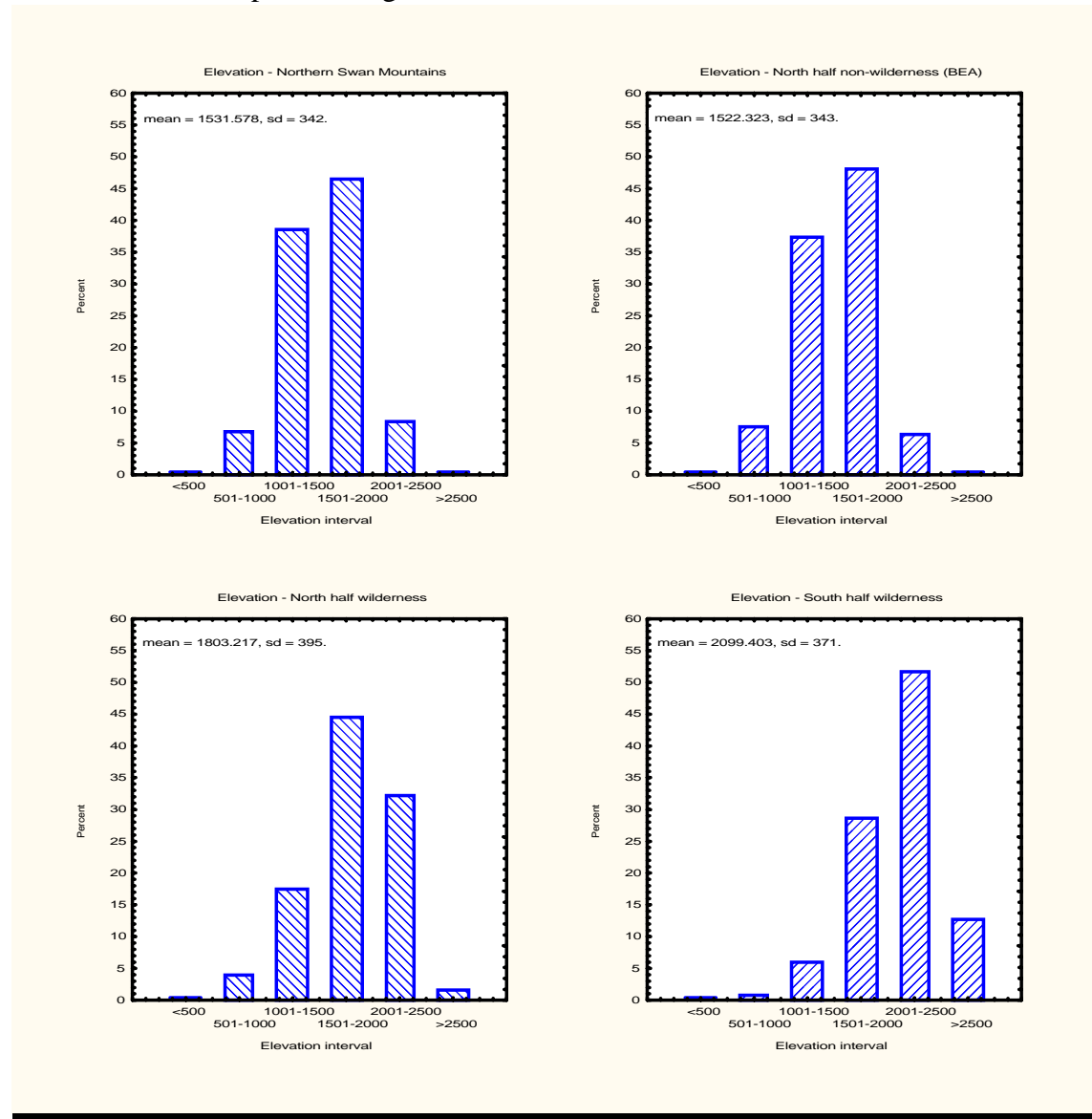
Spectral class diversity – a measure of vegetation diversity also derived from TM satellite imagery (described in Manley et al. 1992). The same scenes were used as were used for greenness.

Figure 3. Spectral class diversity in the northern Swan Mountains reference area and each of the 3 extrapolation regions. The ordinate axis refers to the percent of area within each diversity class.



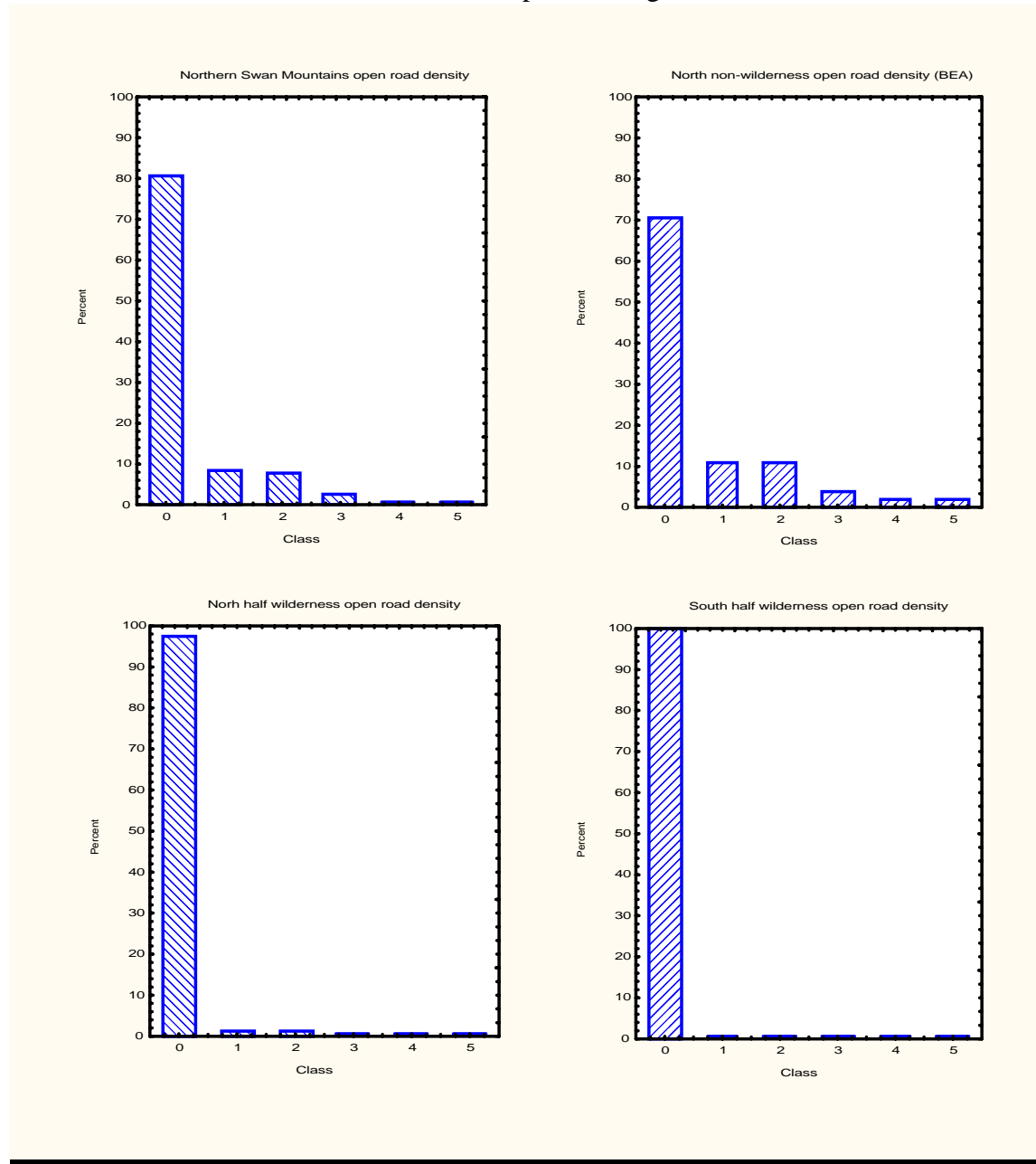
Elevation - measured in meters (from DEM data). Mean elevation in the north half Selway - Bitterroot is higher than in the South Fork Flathead. To adjust for this elevation difference, we subtracted the difference in means (271 m) from the Selway – Bitterroot DEM values.

Figure 4. Distribution of elevation classes in the northern Swan Mountains reference area and the 3 extrapolation regions.



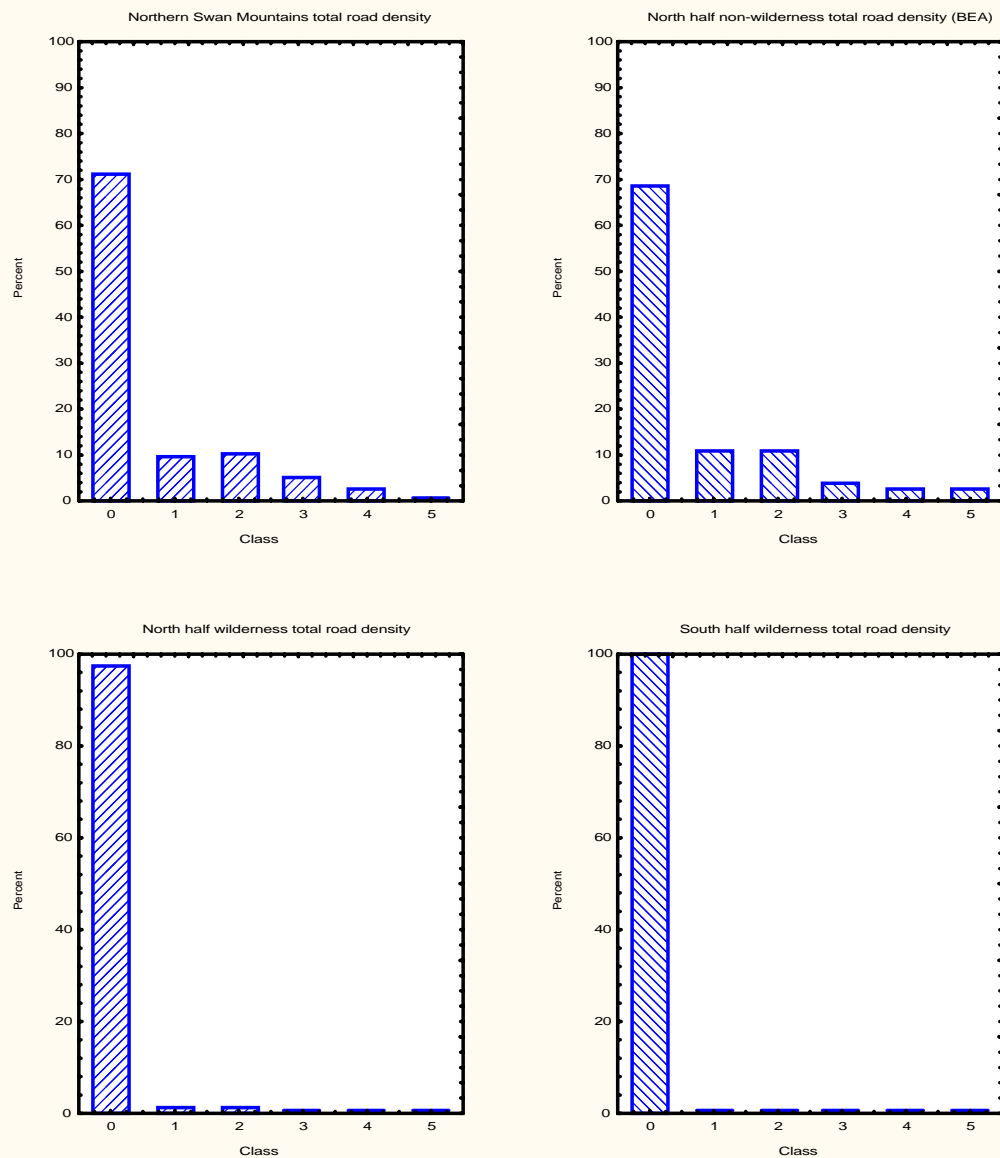
Open road density - measured using the moving windows technique in 5 classes of increasing density in km/km² (as described in Mace et al. 1996). Roads open during any portion of any season were considered open for the year. Digital road maps were obtained from the USDA Forest Service and classified as open or closed according to the Travel Management Record System.

Figure 5. Distribution of open road density classes within the northern Swan Mountains reference area and within each of the 3 extrapolation regions.



Total road density – also measured using the moving windows technique in 5 classes of increasing density in km/km^2 (as described in Mace et al. 1996). All open and closed roads were included in this category.

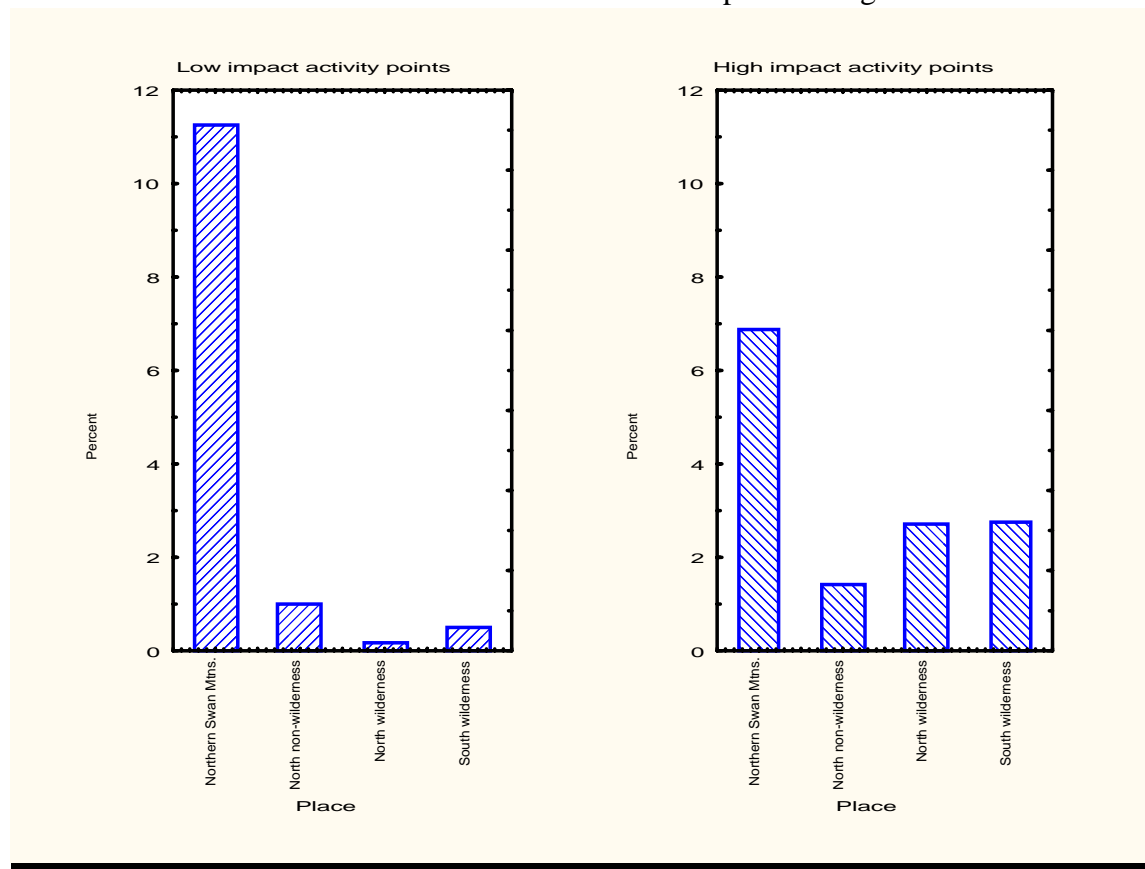
Figure 6. Distribution of total road density classes in the northern Swan Mountains reference area and within each of the 3 extrapolation regions.



Low impact activity points – points where activities thought to have minimal impacts on grizzly bears occurred (incorporated as described in Mace et al. 1997). Digital maps of point source activities were obtained from the USDA Forest Service and classified according to Northern Continental Divide Ecosystem Cumulative Effects Model guidelines.

High impact activity points – points where activities thought to have large impacts on grizzly bears occurred (incorporated as described in Mace et al. 1997). Both low and high impact points were buffered 500 meters.

Figure 7. Distribution of low and high activity point buffers in the northern Swan Mountains reference area and within each of the 3 extrapolation regions.



We used the computer program CALHOME to calculate seasonal multi-annual 95% adaptive kernel home ranges for 11 female grizzly bears that inhabited the northern Swan Mountains during the period 1988-1994. The home range polygons were then converted to GIS map layers (Waller and Mace 1997). The sum of the pixel-by-pixel (30m) cell values of each of the 7 layers at random locations represented the *availability* of the 7 parameters to each of the 11 bears. Aerial telemetry locations for each of the 11 bears, collected between 1988-1994, were used to quantify seasonal *use* of each of the 7 parameters. Logistic regression was then used to calculate coefficients for each parameter for each bear based on *use* and *availability*. The coefficient for each parameter, averaged across all 11 bears was used in a Resource Selection Function (RSF) that describes the relative probability of use of each combination of the 7 parameters within each season (Mace et al. 1997, Manly et al. 1993). The RSF is then applied to the Selway – Bitterroot data and RSF values mapped for each 30m pixel. The season were spring; den emergence to 15 July, summer; 16 July to 15 September, and fall; 16 September to den entrance.

Yellowstone Habitat Model

A similar approach was taken to estimate RSFs for the Yellowstone ecosystem using radio telemetry locations. In this case, however, radio telemetry locations were compiled (1989-1997) over the entire Yellowstone grizzly bear recovery zone. Habitat variables for which data were available for both the Yellowstone ecosystem and the Bitterroots were:

Greenness – a measure of vegetation reflectance derived from Thematic-Mapper satellite imagery, analogous to leaf area index. To produce the Selway – Bitterroot greenness layer, we performed the tasseled cap transformation on TM scene p41r29 in the same manner as in the Yellowstone ecosystem.

Brightness – another measure of vegetation reflectance derived from Thematic-Mapper satellite imagery, brightness is often dominated by the amount of bare ground. Therefore we expect the coefficient to be negative because large brightness values do not indicate areas containing forage for bears.

Wetness – similar to greenness and brightness this measure is also calculated using the tasseled cap transformation of the TM imagery.

Distance to the nearest road (road) – measured in meters. All open and closed roads were included

Elevation – measured in meters (from DEM data). Mean elevation in the south half of the Selway - Bitterroot is lower than in the Yellowstone ecosystem. To adjust for this elevation difference, we added the difference in means (710 m) to the Selway – Bitterroot DEM values.

RESULTS

Bitterroot Habitat Model

The seasonal RSF equations based on the Swan Mountains analysis were:

Spring: $w = \exp(0.25850 + (\text{greenness} * 0.14633) + (\text{diversity} * 0.03205) + (\text{elevation} * -0.00173) + (\text{open road density} * -0.10138) + (\text{total road density} * -0.38789) + (\text{low impact points} * -0.80915) + (\text{high impact points} * -3.39215))$

Summer: $w = \exp(-4.09939 + (\text{greenness} * 0.18133) + (\text{diversity} * 0.04041) + (\text{elevation} * 0.00053) + (\text{open road density} * -0.34569) + (\text{total road density} * -0.23886) + (\text{low impact points} * -0.08599) + (\text{high impact points} * -9.84811))$

Fall: $w = \exp(-4.3707 + (\text{greenness} * 0.15430) + (\text{diversity} * 0.04500) + (\text{elevation} * -0.00070) + (\text{open road density} * 0.19130) + (\text{total road density} * -0.27560) + (\text{low impact points} * -0.57570) + (\text{high impact points} * -10.4967))$

Yellowstone Habitat Model

For the Yellowstone ecosystem we constructed models based on 2 seasons: a spring season prior to 15 July and an autumn season beginning on 15 July. The seasonal RSF equations based on the Yellowstone analysis were:

Spring: $w = \exp\{0.12 * [1 - \exp(-0.00033 * \text{road})] + 0.0017 * \text{greenness} - 0.0011 * \text{brightness} - 0.0022 * \text{wetness} - 0.0006 * \text{elevation} + 0.3886\}$

Autumn: $w = \exp\{0.14 * [1 - \exp(-0.00019 * \text{road})] + 0.002 * \text{greenness} - 0.0068 * \text{brightness} - 0.0024 * \text{wetness} + 0.0017 * \text{elevation} - 4.7905\}$

In both seasons we found models that were statistically significant based on $-2\log$ likelihood criteria ($P < 0.001$).

Population Estimates

Methods outlined in Boyce and McDonald (1999) were used to estimate the population size for the Selway-Bitterroot. We present estimates of the number of grizzly bears for the southern half of the Bitterroots based on both the Swan Mountains and Yellowstone models (Table 6-20).

Table 6-20. Estimates of projected grizzly bear population size based on resource selection function (RSF) models from the Yellowstone ecosystem and the South Fork of the Flathead.

AREA	SPRING	SUMMER	AUTUMN	MINIMUM ESTIMATE
<u>South Wilderness:</u>				
Yellowstone Models	132	---	184	132 (spring)
Northern Swan Mtn. Models	183	126	119	119 (autumn)
<u>North Wilderness:</u>				
Northern Swan Mtn. Models	177	121	115	115 (autumn)
<u>North Non-Wilderness (BEA)</u>				
Northern Swan Mtn. Models	175	74	75	74 (summer)
Estimated total population size using Yellowstone Model:				321
Estimated total population size using Northern Swan Mountains Model:				308

DISCUSSION

We fit the RSF models using logistic regression, which worked fine for the South Fork models. But for the effect of the distance to the nearest road in the Yellowstone model we discovered that the relation was quadratic, i.e., the likelihood of a bear location increased to a maximum and then declined at larger distances. We believe that this observation is a result of bias in the sample of radio-collared bears because bears that inhabited remote country were under-represented. Therefore, rather than retain the quadratic function, we replaced it with an asymptotic function that levels off near the local maximum in the quadratic model. We believe that this is an appropriate adjustment to the model.

Estimates of the number of bears in the Selway-Bitterroot recovery area was highest in spring for both the Yellowstone-based models and the Swan Mountains-based models. This appears to be a

Appendix 21B - Habitat Capability Analysis: Population Potential

consequence of the fact that in the spring models, elevation had a negative coefficient indicating that bears are expected to be more abundant at lower elevations in spring. Because the Bitterroot has proportionately more low elevation habitats than either the Yellowstone or Swan Mountains baseline areas, the spring models indicate more bears even though we adjusted for differences in mean elevation between the Bitterroots and the baseline areas. The Swan Mountains reference area also differed from the extrapolation areas in that greenness and diversity were higher (Figures 6-9 and 6-10), however since coefficients were positive for these parameters, they should reduce the population estimates. Open and total road densities were very similar between the Swan Mountains and the non-wilderness BEA (Figures 6-12 and 6-13). As expected, road densities in the wilderness were lower. The overall effect would be to increase the population estimate as a greater proportion of the extrapolation area in wilderness. The number of low and high-impact activities in the Swan Mountains was substantially more than in the Selway-Bitterroot (Figure 6-14). Again, we would expect this to have a positive impact on the population estimates. Because the population estimates varied, we used the minimum of the annual population estimates for each of the 3 regions in the Bitterroot recovery area reasoning that one season is likely to be limiting to the number of bears.

The estimate of 308-321 bears for the Bitterroot is 10-15% higher than the estimate in the Draft Environmental Impact Statement (USFWS 1997). We expected the number of bears to be lower in the southern ½ of the Bitterroots because generally the habitats are dry and less productive than northern portions of the recovery area. Yet, portions of the Yellowstone ecosystem are also relatively dry and support bears. Even though the forb and berry production in these dry habitats is relatively low, the southern ½ of the Bitterroots contains substantial stands of whitebark pine as well as populations of elk and deer that can provide food for grizzly bears. Certainly the remoteness of the area and the paucity of roads will help to ensure that a viable population of grizzly bears can persist in the Selway-Bitterroot wilderness of Idaho and Montana.

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APPENDIX 21C. METAPOPOPULATION ANALYSIS FOR THE BITTERROOT POPULATION

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One of the early tenets of conservation biology is that population viability is enhanced by maintaining multiple populations of a species (Soulé 1987). Management strategies that reduce variance in population size will also reduce risk of extinction. Asynchrony in population fluctuations in independent populations reduces variance in the aggregate of populations whereas environmental correlation among areas increases the risk that all populations will go extinct (Foley 1994). I use a stochastic model predicting extinction risk to evaluate the decline in the risk of extinction to be had by restoring grizzly bears in the Bitterroot wilderness of Idaho and Montana. Here I quantify the reduced probability of extinction for grizzly bears in the Rocky Mountains of the United States by adding the proposed Bitterroot population.

Only four populations of grizzly bears persist in the conterminous United States: about 420 bears in the Yellowstone ecosystem (Boyce et al. 1999a), 400 in the Northern Continental Divide Ecosystem (NCDE), 40 in the Selkirk Mountains, and 35 in the Cabinet/Yaak Mountains. Although a few grizzly bears are known also to occur in the Cascades of Washington, these animals appear to have dispersed south from Canada and as yet there is no evidence that this is a reproducing population. A proposal to restore a grizzly bear population to the Selway-Bitterroot wilderness of Idaho and Montana could potentially add another population of 308-321 grizzly bears (Boyce et al. 1999c).

Underlying my calculations is a stochastic model from diffusion theory which I use to estimate the probability of extinction during the next 100 years, $P_{ext}(100)$, for each of 4 populations of grizzly bears, and a hypothetical population in the Bitterroots (Foley 1994, 1997):

$$P_{ext}(100) = 1 - \exp\{-100/2n_o[k - (n_o/2)]/V_r\} \quad (1)$$

I require 3 parameters to estimate extinction risk: \log_e of initial population size, n_o ; k , \log_e carrying capacity; and V_r , the variance in the per capita population growth rate, r . With this model I make the conservative assumption that the long-term average growth rate will be approximately 0. Using a larger value of r would usually reduce extinction risk by strengthening density dependence.

The per capita growth rate, $r(t)$, was estimated from a series of grizzly bear population estimates, $N(t)$, for $t = 1, 2, \dots$ by taking the sequential differences in \log_e population sizes between years, i.e., $r(t) = \ln[N(t+1)] - \ln[N(t)]$. I then took the variance of these $r(t)$ values to estimate V_r . My best series of population estimates is from the Yellowstone population, so these were used as the basis for estimating V_r for each population in two ways. First, I used the variance in $r(t)$ from a series of 12 population estimates, 1986-1997, based on cumulative counts of the number of females with cubs of the year (Boyce et al. 1999a). Second, I reconstructed a series of population estimates for 1961-1985 by adding 11.5 to the counts of the number of females with cubs based on the difference between cumulative-count estimates (Boyce et al. 1999a) and actual counts of females with cubs of the year for 1986-1997. Then I used Lowess smoothing (tension = 0.7) to remove trend in the time series (Chambers et al. 1983), and calculated V_r from the residuals of the smoothed series. The first method yields a relatively "high" estimate of V_r because it includes a population increase over the period 1983-1997 (Boyce et al. 1999a). The second method is a relatively conservative estimate because I have removed all trend in population size; I call this a "low" estimate of V_r (see Appendix for summary of definitions). Even though the second method yields relatively low estimates of V_r , both methods actually may overestimate the variance in per capita growth rates because the cumulative counts also reflect variation in reproductive output over time.

For the Yellowstone ecosystem, estimates of density-dependent survival suggest that the current population of 420 is nearing a carrying capacity of about 450 grizzly bears (Boyce et al. 1999b). Carrying

Appendix 21C - BE Habitat Capability Analysis: Metapopulation Analysis

capacity for the Bitterroot population was estimated to be 308-321 using projected populations from an analysis of resource selection functions for the projected recovery zone (Boyce et al. 1999c). Carrying capacities for each of the other populations were approximated by 3 methods: (1) assuming that carrying capacity was equal to the official recovery goal in the Grizzly Bear Recovery Plan (USFWS 1993), (2) assuming that the current population size reflects the long-term carrying capacity for each area except the Bitterroots, or (3) assuming that the Cabinet-Yaak, Selkirk, and NCDE populations are merely the southern extension of a much larger contiguous Canadian bear population. This third approach has the consequence of greatly increasing the population size for the Cabinet-Yaak, Selkirk and NCDE populations, thereby greatly enhancing the joint long-term viability of the United States' populations. These 3 approaches correspond to the numbered section of Table 6-21.

Dispersal, to a point, lowers extinction probabilities. Under simplifying assumptions, Kuno (1981) found that random migration between 2 populations over a wide range of environmental fluctuations had the effect of lowering the variance in rate of population change, V_r , by $1/(\text{number of populations})$. I assumed that dispersal was possible, but only between the 4 northern sites, NCDE, Selkirks, Cabinet/Yaak Mountains, and the Bitterroots. I presumed that the Yellowstone would remain independent due to the distance between it and the others. Thus for the northern 4 populations I multiplied the variance by $1/4$ to account for the fact that we have 4 populations amongst which dispersal might occur—an optimistic assumption without management intervention (Servheen et al. 1995). For the second option where I assumed that populations would not increase to management objectives, I assume that dispersal will occur only among 3 populations: Selkirks, Cabinet/Yaaks, and the Bitterroots.

For the calculations presented in Table 6-21 I ignored the possible consequence of correlation among areas because I have empirical evidence for such a correlation. If such a correlation is identified, the extinction risk would increase. Indeed, if grizzly bear populations decline due to continued habitat loss, such a correlation will almost certainly occur. At the extreme, if the correlation were 1.0, the extinction risk would be equal to the extinction probability of the population with the lowest risk of extinction. If correlation is 0, the risk of extinction is the product of the independent probabilities of each subpopulation. For intermediate environmental correlation, if I assume that increasing correlation is linearly related to extinction risk, a model for estimating extinction probability with environmental correlation $P_{ext-cor}$ is:

$$P_{ext-cor} = P_{ext(all)} + (P_{ext-min} - P_{ext(all)})R^2 \quad (2)$$

where $P_{ext(all)}$ is the joint extinction probability of all the populations if they were independent, $P_{ext-min}$ is the extinction probability of the most persistent population, and R^2 is the coefficient of determination between/among populations. Equation 2 yields a function where $P_{ext-cor}$ decreases as number of populations increases but quickly reaches an asymptote that is determined by the degree of correlation.

Generally, the probability of extinction for the entire assemblage of grizzly bear populations is very low, being $3/1,000$. One must view these estimates cautiously because there is great uncertainty in the estimates (Ludwig 1999). Also, one must also question whether the probability of extinction is an appropriate measure to consider in a conservation context. In fact, resource managers already are committed to manage to achieve viable populations of grizzly bears larger than exist now (U.S. Fish and Wildlife Service 1993). Nevertheless, for comparative purposes I believe that the estimates are useful.

The results of my calculations predict that the addition of the Bitterroot population will reduce the probability of extinction by 88-99% depending on the variance in r . I was surprised that the relative change in extinction probability was about the same whether I assumed a baseline K equal to the projected recovery targets, or estimated number of bears in the entire ecosystem including bears from Canada. Adding additional populations causes a geometric decline in extinction probability, and greatly improves the

probability of existence and therefore the effectiveness of conservation for the grizzly bear.

Table 6-21. Extinction probability for Rocky Mountain grizzly bear populations in the United States as influenced by the addition of a population in the Bitterroot wilderness of Idaho and Montana. The model assumes dispersal among the Northern Continental Divide Ecosystem (NCDE), Selkirk Mountain, and Cabinet-Yaak Mountain populations. Carrying capacities for the first 3 areas are set first at the recovery goals, then at current population sizes, and finally at levels that include Canadian extensions of the 3 northern populations.

(1) Assuming k = recovery targets for each population					
Variable	NCDE	Selkirks	Cabinet/Yaak	Yellowstone	Bitterroot
N	400	40	35	420	25
$n(0)$	5.992	3.689	3.555	6.04	3.219
K	500	106	106	450	308
k	6.215	4.663	4.663	6.109	5.73
V_r (high)	0.0243	0.0243	0.0243	0.097	0.0243
$P_{ext}(100)(\text{high } V_r)$	0.061	0.110	0.112	0.229	0.087
V_r (low)	0.0025	0.0025	0.0025	0.01	0.0025
$P_{ext}(100)(\text{low } V_r)$	0.0065	0.012	0.012	0.026	0.009
			Low V_r	High V_r	
$P_{ext}(\text{all})$			2.318x10 ⁻¹⁰	0.000015	
<i>odds</i>			2/10 billion	15/1 million	
$P_{ext}(\text{all})$ (without Bitterroots)			2.472x10 ⁻⁸	0.000171	
<i>odds</i>			2/100 million	17/100,000	
Improvement in P_{ext} with Bitterroots			99.1%	91.3%	

Appendix 21C - BE Habitat Capability Analysis: Metapopulation Analysis

(2) Assuming $k = n(0)$ and no interchange with NCDE

Variable	NCDE	Selkirks	Cabinet/Yaak	Yellowstone	Bitterroot*
$P_{ext}(100)(\text{high } V_r)$	0.237	0.212	0.226	0.234	0.115
$P_{ext}(100)(\text{low } V_r)$	0.028	0.024	0.026	0.027	0.013
		Low V_r		High V_r	
$P_{ext}(\text{all})$ <i>odds</i>		5.841x10 ⁻⁹ 6/1 billion		0.000303 3/10,000	
$P_{ext}(\text{all})$ (without Bitterroots) <i>odds</i>		4.677x10 ⁻⁷ 5/10 million		0.00264 3/1,000	
Improvement in P_{ext} with Bitterroots		98.8%		88.5%	

* for Bitterroot population $k = \ln(308)$

(3) Assuming K includes Canadian populations

Variable	NCDE	Selkirks	Cabinet/Yaak	Yellowstone	Bitterroot
K	2000	1000	1000	450	308
$P_{ext}(100)(\text{high } V_r)$	0.0411	0.0496	0.0496	0.2289	0.0874
$P_{ext}(100)(\text{low } V_r)$	0.0043	0.0052	0.0052	0.0264	0.0094
		Low V_r		High V_r	
$P_{ext}(\text{all})$ <i>odds</i>		2.924x10 ⁻¹¹ 3/100 billion		2.018x10 ⁻⁶ 2/1 million	
$P_{ext}(\text{all})$ (without Bitterroots) <i>odds</i>		3.117x10 ⁻⁹ 3/1 billion		0.000023 23/1 million	
Improvement in P_{ext} with Bitterroots		99.1%		91.3%	

Appendix. Variable definitions.

K	carrying capacity where $dN/dt = 0$
k	\ln carrying capacity
N	population size
n	\ln population size
$P(100)$	probability of persistence over a 100-yr time interval
P_{ext}	probability of extinction
$P_{ext}(100)$	probability of extinction within 100 years
$P_{ext(\text{all})}(100)$	joint probability that all populations go extinct within 100 years
r	per capita growth rate
t	time
V_r	variance in r

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**APPENDIX 21D. EXCERPTS FROM AND SYNOPSIS OF PORTIONS OF
THE REPORT, “*Abundance and Spatial Distribution of Grizzly Food-Plant
Groups in the Salmon-Selway Ecosystem: A Preliminary Analysis and Report*”
(Hogg, Weaver, Craighead et al. 1999)**

BACKGROUND

The Craighead Wildlife-Wildlands Institute (CWWI) of Missoula, Montana initiated a vegetation-based inventory and analysis of grizzly bear habitat in the Bitterroot Ecosystem in the fall of 1995 partially in response to the USFWS Notice of Intent and Scoping for a proposal to recover grizzly bears in the Bitterroots. The inventory and analysis utilized Landsat Thematic Mapper satellite imagery and on-the-ground botanical surveys. Part of the goal was to determine distribution and abundance of grizzly bear food plants for the entire ecosystem. Existing habitat studies including Scaggs (1979), Butterfield and Almack (1985), and Davis and Butterfield (1991) evaluated only portions of the ecosystem and used different methods.

Public comments on the Draft Environmental Impact Statement (EIS) indicated a general concern about the adequacy of habitats for grizzly bear recovery in the Bitterroot Ecosystem. To be responsive to public comments, the USFWS decided to improve the habitat information for the Final EIS. The USFWS approached the CWWI and coauthors about incorporating some of their results into the Final EIS. The USFWS met with CWWI researchers and their colleagues over a 20-month period to share information, review preliminary analyses and results, and discuss ways in which information from their project might be used in the Final EIS.

This appendix, prepared by the USFWS, **excerpts** portions of their preliminary report, “*Abundance and Spatial Distribution of Grizzly Bear Food-Plant Groups in the Salmon-Selway Ecosystem: A Preliminary Analysis and Report*” (Hogg, Weaver, Craighead et al. 1999). It contains only portions of the report pertinent to the Final EIS and to concerns raised by public comments on the Draft EIS. The CWWI and coauthors have granted the USFWS permission to reproduce the “Introduction,” “Study Area” and “Methods” sections verbatim from their report as well as a subset of three tables (reproduced with minor modifications) and three figures containing results. In this appendix, the reproduced tables and figures are labeled Table 6-22, 6-23, and 6-24 and Figure 6-15, 6-16, and 6-17. The appendix has been reviewed for technical accuracy by the CWWI and coauthors. However, interpretations of the results made by the USFWS may not necessarily represent the views or conclusions of the CWWI or individual authors.

Hogg, Weaver, Craighead et al. (1999) present preliminary information on the abundance and spatial distribution of key grizzly bear foods in the Bitterroot Ecosystem. For information about their preliminary report (referred to in this appendix) and related documents, contact the Craighead Wildlife-Wildlands Institute, 5200 Upper Miller Creek Road, Missoula, Montana 59803.

The USFWS would like to express gratitude to the Craighead Wildlife-Wildlands Institute and colleagues for their cooperation and permission to reproduce portions of their report.

INTRODUCTION

This “Introduction” section is reproduced verbatim from Hogg, Weaver, Craighead et al. (1999) with the permission of the authors:

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Craighead (1976) and Craighead, Sumner and Scaggs (1982) first proposed, developed, and applied methods for combining botanical survey (ground truthing) and Landsat TM imagery to map wilderness vegetation and delineate critical habitat on an ecosystem scale. The first "ecospectral" vegetation map was produced for a 204 km² primary study area in the Scapegoat Wilderness of northwestern Montana, validated with additional ground truthing in two secondary study sites, and then extrapolated with excellent accuracy to more than 4500 km² of surrounding terrain. Although the map was developed with primary reference to grizzly bear habitat requirements, the authors explicitly recognized and advocated the much broader potential application of landscape scale vegetation maps in conservation (see also Craighead 1982; Craighead, Craighead and Craighead 1986). These methods were refined and tested in the Kobuk River region of Alaska, an arctic ecosystem with markedly different plant associations and geology (Craighead, Craighead, Craighead et al. 1988). The Kobuk River vegetation map was subsequently combined with new techniques for satellite remote-sensing of animal location (Craighead and Craighead 1987) to monitor and describe grizzly bear habitat use in the ecosystem (Craighead 1998). The close historical connection between the development of methods for satellite-aided vegetation mapping and grizzly bear habitat evaluation was no accident. The methods are particularly appropriate for species, like the grizzly, that have space-intensive life histories and prefer or require wilderness landscapes (Craighead, Sumner and Mitchell 1995).

Our current studies in the Salmon-Selway Ecosystem are part-and-parcel of a long-term Craighead Wildlife-Wildlands Institute (CWWI) research program, initiated and enabled by these earlier mapping studies, in which an overarching goal is a remote-sensing aided inventory and evaluation of grizzly bear habitat throughout the Northern Rockies (Craighead 1982). Our decision to focus on the Salmon-Selway followed directly from a specific suggestion made within this broader vision by Craighead (1982, p. 22); the work has taken on special urgency in view of ongoing plans by the U.S. Fish and Wildlife Service to repatriate grizzly bears to this still wild and remote region. We have taken full advantage of improved methods of mapping arising during a virtual explosion of remote-sensing applications in the last decade (including some provided by authors of the current report). However, the fundamental elements of ecosystem mapping have remain unchanged. We have also retained, from the first mapping studies, the core philosophy that remote sensing is an aid to, not a replacement for, on-the-ground field biology. Remotely sensed data have limited value to conservation until supported by heavy investment in field-based surveys designed to define, guide, and validate ecological classifications of landscapes at large spatial scales (Craighead 1980).

STUDY AREA

This "Study Area" section is reproduced verbatim from Hogg, Weaver, Craighead et al. (1999) with the permission of the authors:

Conceptually, our study area was the Salmon-Selway ecosystem (Figure 6-15). This 100,000 km² complex of mountains, foothills, canyons and river valleys is centered on the broad back of the Idaho Batholith. The ecosystem is approximately bounded by the Snake River plain to the south, Hells Canyon and the Palouse prairie of the Idaho panhandle to the west, the Missoula and Clark Fork River valleys in the north, and the Bitterroot Mountains to the east. Technically, the study area was defined by the boundaries of Landsat TM scenes P41R28 (dated July 20, 1991) and P41R29 (dated July 31, 1995) which together cover the majority of the area of conceptual interest.

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Two major rivers have their headwaters in the Salmon-Selway: the Selway River in the north and the Salmon River in the south. Tributaries of the Snake, Clearwater, Bitterroot and Clark Fork Rivers drain the southern, western, eastern and northern fringes of ecosystem, respectively. The northern portion of the Salmon-Selway is characterized by a Pacific Maritime climate and features an expanse of relatively mesic, montane forest and shrublands above which rise the island-like peaks and alpine plant communities of the Selway Crags and Bitterroot Mountains. In contrast, the more uniformly rugged, mountainous terrain of the southern Salmon-Selway is influenced by an arid Basin and Range weather pattern and displays a more complex mosaic of grass, shrub and forest plant community types. The transition between these broad ecological zones of the ecosystem is fairly abrupt and roughly coincides with the area of overlap between the northern and southern TM scenes.

METHODS

This “Methods” section is reproduced verbatim from Hogg, Weaver, Craighead et al. (1999) with the permission of the authors:

Sources of Botanical Data: *We used botanical data from four sources: (i) Craighead Wildlife-Wildlands Institute (CWWI) (collected 1996-98); (ii) Forest Service (FS) Region 1 (collected 1994-95); (iii) FS Intermountain Fire Sciences Lab (collected 1995) and (iv) FS Region 4 (compiled 1996). Data from these sources varied in terms of the collection method and information recorded. CWWI and FS Region 1 data featured more comprehensive field plots located in and around wilderness cores, whereas Region 4 botanical data were more apt to be peripherally located in multiple use areas, missing data of interest to us (e.g., habitat type or species composition lists) and/or based upon photo interpretation rather than field inventory. A total of 3595 and 5929 training plots were used to classify TM scenes P41R28 and P41R29, respectively.*

Pooling data collected by different groups for different reasons was not our preferred method. However, the large size of the area and ongoing planning for repatriation imposed sample size targets and time constraints that we could not otherwise meet. Our accuracy assessment suggests that more was gained than lost by pooling.

Botanical Sampling Design: *CWWI training plot locations were chosen via a hierarchical process and according to both ecological and spectral criteria. We first stratified the ecosystem into broad biogeographic regions which, based on topographic and climatic considerations, could reasonably be expected to capture most of the ecological diversity in the study area. These regions included the arid canyon country of the middle and main forks of the Salmon River, mountain massifs such as the Bighorn Crags and Sawtooth Mountains, the broad, upland basin of Chamberlain Creek and the mesic forest lands of the upper Lochsa and Selway Rivers and their tributaries. Within each biogeographic region, we then sub-sampled four to six, 60 km² quadrangles corresponding in size and boundaries to 7.5 minute, USGS topographic maps.*

In 1996-97, quadrangles were selected for high ecological diversity, high spectral diversity as revealed by the TM imagery, or both characteristics. We used our knowledge, and that of others familiar with a particular bioregion, to identify quadrangles having high ecological diversity and a mathematical algorithm developed by the Wildlife Spatial Analysis Lab to rank quadrangles by spectral diversity. Plot placement within selected quadrangles was largely driven by spectral information. First, we located plots so that most

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if not all spectral classes represented on the TM image of the quadrangle in question were sampled. Second, we generally selected areas that were spectrally homogenous; plots were usually placed within polygons (map regions) in which 70-80% of the polygon's constituent pixels were classified to a single spectral class. However, in areas where spectral heterogeneity was widespread and appeared to reflect vegetational mosaics, we did not select for monotypic polygons. We used topographic maps, TM imagery and Global Positioning Systems (GPS) (GeoExplorers, Trimble Navigation, Inc.) to navigate to polygons selected for plot location. One-tenth acre plots were laid out 100-120 m (3-4 pixels) in from the polygon border at a point judged to be representative of vegetation in the polygon as a whole. We did not place plots in polygons of the same spectral class that were separated by less than 500 m. However, replicate plots in the same polygon from different data sources were allowed.

In 1998, quadrangles and plot locations were chosen randomly with respect to spectral pattern as follows. We first identified quadrangles within biogeographic regions and sampling areas within quadrangles that captured major landform features (canyons, ridges, etc.) in rough proportion to their areal extent in the larger area (biogeographic region or quadrangle). Access (e.g., via trail systems) as well as landform variety influenced the size, shape and location of sampling areas within quadrangles. Transects were laid out within sampling areas. Transect origin along an access route was determined by selecting a random number between 300 and 1000 and walking that number of meters from the start of the access route (or origin of the previous transect). Transect bearing (azimuth) was similarly determined by selecting a random number between 0 and 360 (degrees). Finally, location of one-tenth acre plots along a transect with fixed origin and bearing was determined by selecting a random number between 100 and 500 and walking that number of meters from the transect origin (or previous plot). In contrast to 1996-97, replicate CWWI plots within the same polygon were permitted. All plots were again GPS-located.

Plot Data: *Both the data collected on CWWI's plots and the method of measurement were modeled on FS Region 1 Ecodata because we anticipated combining our plot data with existing data of this type. Some traditional Ecodata fields (e.g., related to fuel load) were not directly relevant to our application and were not collected in all years. We will ignore these data in this report, but readers should be aware that they exist for some plots.*

CWWI plot data consisted of (i) quantitative data on plant species composition, coverage and vegetative structure and (ii) categorical variables, or labels, designating membership in a recognized plant community type. For all plots in all years, we estimated percent coverage (0-100%) for each plant species known to be a grizzly bear food.

*Whitebark pine nuts are an important, if variable, source of food for grizzlies in late summer and autumn (Craighead, Sumner and Scaggs 1982). Because there is widespread concern that cone-producing whitebark trees are in decline in the Northern Rockies from infestations of white pine blister rust fungus (*Cronartium ribicola*) and mountain pine beetle (*Dendroctonus ponderosae*), we recorded some additional data for plots in whitebark pine stands. In 1996, we initially used a condensed, and slightly altered, version of methods designed to standardize data collection for studies of whitebark pine status in the Northern Rockies (Kendall 1995). However, these methods were time consuming (involving many measurements of each whitebark tree on plot) and consequently at odds with our primary objective of obtaining large numbers of training plots for map production. Thus, in the latter part of 1996, we limited complete measurements to 15 whitebark pine trees per size class and, in 1997, we further reduced extra data collection on whitebark plots. Measurements*

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on whitebark pine made in both years were (i) size class and height, (ii) percent cover, (iii) presence or absence of cones, (iv) number of live and dead trees per plot, and (v) notes on blister rust infection. In 1998, (i)-(v) were recorded on 43 plots and (ii) and (v) on the remaining 1083 plots.

Ecological Classification System: A land cover classification system is sometimes defined as a set of categories in which each land cover category identifies either a non-living surface material (e.g., barren ground, snow field, etc.) or a distinctive association of plant species. However, we follow Craighead, Craighead, Craighead et al. (1988) in using “land cover type” to refer to categories defined by non-vegetative features (rock, water, etc.) and either “plant community type” or “vegetation complex” to refer to categories defined by vegetative features (below). Botanical plots in vegetated areas were assigned membership in a hierarchical system of vegetation categories that was based upon (i) a modification of the Montana and Idaho Vegetation and Land Cover Classification System (1997) developed in consultation with agency and academic ecologists by the Wildlife Spatial Analysis Lab, and (ii) the USDA Forest Habitat Type System. Most of the forest lands in P41R28 fell under the Northern Idaho Forest Habitat Type System (Cooper, Neiman and Roberts 1991) whereas those in P41R29 fell under the Central Idaho Forest Habitat Type System (Steele, Pfister, Ryker et al. 1981).

Non-forest plots and the forest canopy of forest plots were classified according to the Montana and Idaho Vegetation and Land Cover Classification System. The first level in this classification was general lifeform (forest versus non-forest). Forest and non-forest areas were divided at additional levels by ecological, specific lifeform and taxonomic criteria. The final level was defined by dominant or co-dominant plant species. Not all branches in the classification system divide at every level. This is because (i) some levels of subdivision do not logically apply to all branches or (ii) a subdivision, though possible, has not been developed. We follow Craighead, Craighead, Craighead et al. (1988) in referring to categories at the final level as non-forest or forest canopy plant community types and to higher level groupings of plant community types as non-forest or forest canopy vegetation complexes.

The understory (all non-canopy strata) of forest plots was categorized separately according to the Forest Habitat Type System. Following the terminology presented above, we refer to understory habitat types as understory plant community types and groupings of two or more understory plant community types as understory vegetation complexes.

In summary, our ecological classification of training plots included non-forest, forest canopy and forest understory plant community types which were sometimes grouped into vegetation complexes (non-forest, forest canopy, and forest understory) for purposes of mapping. We emphasize that we described and mapped existing vegetation in all cases. The habitat type classification system, which includes information on potential vegetation as well, was used only to describe existing understory plant associations.

Data Management: CWWI plot data were entered into FoxPro databases using custom data entry screens and custom error- and logic-check routines. Error checks flagged entries that were outside the range of possible values for a given field. Logic checks flagged entries in two or more fields that were incompatible (one or more impossible entries given the value of the others). We checked flagged entries against the field data forms and corrected errors whenever possible. Plot data from FS Region 1 and Fire Sciences Lab (but not Region 4) sources were subjected to a similar battery of error and logic tests. Region 1 plots with errors having an obvious correction (i.e., spelling or typographical errors) were corrected and retained. If errors

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existed but corrections were not obvious, we discarded these plots. We differentially corrected latitude and longitude recorded for CWWI plots in GPS rover files with Pathfinder software using base station files from the appropriate base station (Idaho City, McCall or Missoula). Region 1 and Region 4 plots were differentially corrected by the agency.

We examined plots from all sources for statistical outliers in spectral values and removed 328 (P41R28) and 496 (P41R29) outlier plots from the data set. We moved 249 (P41R28) and 104 (P41R29) training plots located within 1-2 pixels of their polygon boundary into an adjacent polygon because the spectral signature of the initial polygon did not match the general lifeform (forest versus non-forest) of the plot. Such mismatches are attributable to measurement error in GPS-derived locations. Finally, we removed from the data set 1317 Region 4 plots located within clear cuts but assigned by the agency to a (potential) forest canopy plant community type. Plots that fell within polygons belonging to manually-labeled land cover classes (urban, agriculture, water, snow, cloud, cloud shadow) were also deleted.

Unsupervised Map: The Landsat TM images had a resolution of 30 m. Each 30 x 30 m pixel carried a unique combination of values for seven TM channels (1, 2, 3, 4, 5, 6 and 7) as measured by sensors aboard the Landsat satellite. Mathematical algorithms developed by the Wildlife Spatial Analysis Lab were used to assign each pixel to one of approximately 130 spectral classes depending on its values for TM channels 3, 4 and 5. Pixels were then aggregated (merged) into polygons that had a five acre (22 pixel) or one acre (4 pixel) minimum size (minimum mapping unit) depending on whether the area was upland or riparian, respectively. The spectral class assigned to the polygon as a whole was the spectral class in the majority among member pixels. We will refer to the unmerged spectral map of pixels as the pixel image and the merged spectral map of polygons as the unsupervised image.

Spatial Classifiers: A classifier is a statistical procedure for using training (plot) data to predict membership of unclassified data. For vegetation mapping using remotely sensed data, classifiers are used to predict plant community type or vegetation complex membership for all polygons delineated in an unsupervised Landsat TM image. Classification is accomplished by comparing the attribute values of a given unclassified polygon to those of the (classified) training data. More specifically, we used k-nearest neighbor classifiers (Steele and Patterson 1998) to determine the similarity of unclassified polygons and the classified training data based on the attribute values. The k-nearest neighbor classifiers provided initial estimates of the probability of membership in each vegetation complex. These initial estimates were then modified using spatial information conveyed by the vegetation group memberships of training data that were geographically near a given unclassified polygon (Steele and Redmond 1998). Finally, the unclassified polygon was predicted to be a member of the vegetation complex with the largest modified probability of membership. Polygon attributes used in classification were TM bands 1-7, M_NDVI, elevation, slope, slope/aspect, latitude and longitude. M_NDVI is a function of TM bands 3, 4 and 5 (Nemani, Pierce, Running et al. 1993). Slope/aspect is an index of insolation calculated from slope and aspect. Spatial classifiers improved our accuracies in classification (percent correct assignments) by 10 to 15% over conventional classifiers.

Supervised Map: Training data and spatial classifiers were used to classify each unsupervised image independently in a hierarchical sequence of three steps. These steps broadly reflect the structure of our ecological classification (above). First, we assigned polygons to lifeform (forest versus non-forest). Second, we classified non-forest polygons to one of 8 (P41R28) or 7 (P41R29) non-forest vegetation complexes and forest polygons to one of 7 (P41R28) or 8 (P41R29) forest canopy vegetation complexes (Table 6-22).

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Finally, forest polygons were also classified into one of eight understory vegetation complexes (habitat type groups) (Tables 6-22 and 6-23). Water, snow, cloud, cloud shadow, urban, and agricultural areas were manually labeled. Most burns were first manually labeled and then assigned to one of two burn-related vegetation types (conifer regeneration dominated or shrub-herbaceous dominated burn) with a spatial classifier. After classification, the two images were edge-matched.

The number of non-forest, forest canopy and forest understory vegetation complexes that we mapped was always less than the number of plant community types that we recognized in the collection of the plot data. This was because not all plant community types could be mapped with acceptable accuracy by our methods. We created predictable and ecologically coherent vegetation complexes by grouping plant community types that were difficult to distinguish spectrally but ecologically similar. Because the non-forest/forest canopy ecological classification was hierarchical (above), we agglomerated, when necessary, non-forest and forest plant community types into vegetation complexes simply by moving up levels in the classification until the overall accuracy of the supervised map, and that of each component plant community type or vegetation complex, was acceptable.

The procedure for grouping understory plant community types (habitat types) into understory vegetation complexes (Steele, Hogg and Redmond; in preparation) was more complicated. Step one involved making an initial grouping of eight to nine complexes based purely on an evaluation of ecological similarity. Each understory complex constituted a unique collection of habitat types, and each habitat type was assigned to a single complex. We then used the training plots to formulate predictive rules for classifying polygons to understory vegetation complex. Attributes examined for their predictive ability in this procedure were the seven TM spectral bands, M_NDVI, elevation, slope and slope/aspect. We estimated the overall accuracy of the predictive rules using leave-one-out cross-validation (McLachlan 1992; see next section). In addition to this overall accuracy rate, we used leave-one-out cross-validation to calculate the frequency at which training plots belonging to a specific understory type were predicted to be a member of each initial understory vegetation complex. This calculation gave an assessment of the fidelity of each understory type to each (provisional) understory complex. We then revised the grouping of understory plant community types into understory vegetation complexes with the objective of maximizing the rate at which polygons of a known understory plant community type were predicted to belong to its parent understory complex. For example, if polygons known to belong to a particular understory plant community type were consistently predicted to belong to a complex different from the one to which that understory type was initially assigned (its initial parent complex), we re-assigned the understory type to another parent complex—provided that the ecological integrity of the understory system was maintained. The entire process of accuracy assessment and understory complex revision was repeated until no further revisions were obvious.

Briefly, 123 (P41R28) and 88 (P41R29) habitat types represented in training plots were grouped into eight (four per scene) understory vegetation complexes. However, 48 and 35 habitat types in P41R28 and P41R29, respectively, accounted for roughly 80% of the understory training set. These common types had greater influence in classification and they were also given greater weight in our ecological characterization of the understory complexes. Because of the ecological breadth of the understory complexes, no two- or three-word description adequately captured the ecological linkages between habitat types within an understory complex. Therefore, we created numeric labels to be used when brevity is important and indexed the numeric labels to a four-term, descriptive clause appropriate to each understory complex. The first term in these descriptions reflects temperature class (hot, warm, cool, cold), the second moisture class (dry, moist,

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wet), the third indicator species and the fourth characteristic tree species (Table 6-23).

The number and types of non-forest, forest canopy and forest understory vegetation complexes mapped in P41R28 versus P41R29 (Table 6-22) are somewhat different for two reasons. First, there were distinct plant associations (plant community types) that were present in the more mesic north but not in the arid south, and vice versa. Secondly, because of differences between scenes in numbers of training plots and/or our ability to distinguish the spectral signature for plant associations occurring in both scenes, we sometimes grouped differently to maintain our minimum standard of mapping accuracy. The edge-match boundary (Figure 6-15) marks the division between polygons classified according to the northern versus southern ecological classification. The edge-match boundary is irregular because it followed polygon boundaries (a polygon must be classified according to one and only one system).

Classification Accuracy: *We evaluated classification accuracies by leave-one-out cross-validation (McLachlan 1992). Our application of cross-validation involved removing the first training observation from the training set and constructing a new classification rule from the reduced training set. This new rule was then used to classify the polygon containing the left-out training observation. The process was repeated until all observations were held out once and used as a singleton test set. The estimated accuracy rate was the percentage of (held-out) observations correctly classified. A correct classification was one in which the vegetation type predicted for a polygon matched that assigned to the training plot present within the polygon. We also examined and displayed the spatial pattern of classification accuracy using the technique of Steele, Winne and Redmond (1998).*

Estimating Coverage of Grizzly Bear Food-Plant Groups: *The species defining non-forest, forest canopy and forest understory complexes in our ecological classification are not always or even often bear foods (the mixed whitebark pine forest canopy complex is an exception). We used the methods of Steele, Hogg and Redmond (in preparation) to provide an alternative classification of scenes P41R28 and P41R29 that more directly reflects the food-plant resource dimension of the grizzly bear niche. The essence of their approach is to combine remote-sensing data, plot data, supervised land cover maps, and regression analysis to build predictive models for attributes that have been explicitly defined or selected to reflect some aspect of habitat suitability for the species of interest. In our application of that approach, we built predictive models for the collective areal coverage of plant species assigned to five grizzly bear food-plant groups: primary berries, secondary berries, nuts, tubers and stems/leaves/flowers. In inferring food abundance from coverage values, we assume that the areal extent of above-ground vegetative structure on the one hand, and the productivity of reproductive (berries, nuts) and below-ground storage structures (tubers) on the other, respond similarly to variation in soil moisture, canopy closure and other potential limiting factors.*

*Our list of bear food-plant species was assembled from the literature on bear food habits (for a recent review, see Craighead, Sumner and Mitchell 1995). It is not necessarily comprehensive. For example, there are no grizzly food habit studies from the Salmon-Selway ecosystem; plant species that are absent or rare elsewhere could be significant bear foods here. Assignment to food-plant group was based upon evaluation, using the same literature, of the plant part(s) eaten and, in the case of primary versus secondary berries, their relative importance in the grizzly diet. Species utilized for more than one plant part (e.g., tuber and stems/leaves/flowers of *Lomatium* spp.) were counted in the more nutritious food group (e.g., *Lomatium* spp. were counted in the tuber group).*

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Predictive models were built as follows: First, for each CWWI training plot, we summed coverage values recorded for all plant species belonging to a given food-plant group to get a plot-specific estimate of the collective coverage of species in that group. We repeated this summation for all food-plant groups yielding five estimates of collective coverage for each training plot (one for each food group). Second, we identified potential predictor variables measured on plot (forest canopy vegetation complex) or otherwise available for the polygon within which a training plot was located (TM bands 1-7, slope, slope/aspect and elevation). Third, we used multiple regression to estimate the linear relationships between the predictor variables and the coverage of a particular food-plant group. Coverage was predicted as a continuous variable over the range 0-100%. We used the arcsine-square root transformation (Snedecor and Cochran 1980, p. 290) of coverage values in regression analysis. Predicted values were transformed back to the original 0-100% scale for display in tables via the inverse transformation. Separate models were built for each food group in each scene and, within food groups, for each of the four forest understory vegetation complexes and for three ecological groupings of the non-forest vegetation complexes mapped in P41R28 and P41R29. Thus, there were a total of 14 models per food group. A backward step-wise variable selection method was used to select predictor variables. Variables that were significant at the 0.05 significance level were retained in the predictive model. Residuals from the fitted regression model were checked for spatial autocorrelation by constructing a variogram (Cressie 1992, p. 58). No evidence of spatial autocorrelation was found. This result is consistent with our impression that bear food-plant coverage varies substantially over short distances with variation in topography, canopy structure, soils, and moisture availability.

We used this set of models to predict percent coverage of each food-plant group for all polygons (previously classified to vegetation complex as described above) in both scenes. To provide estimates of the total area covered by each food group within the study area, or sub-region thereof, we multiplied these polygon-specific estimates of coverage by the polygon's area and summed these products over all polygons within the region of interest (Table 6-24). To examine the areal distribution within each sub-region across six coverage classes, we summed areas for the subset of polygons predicted by regression to have a coverage value within the range of values defining each coverage class (Table 6-24). Finally, we examined the spatial distribution of coverage classes by assigning each polygon to the coverage class appropriate to its predicted coverage value, labeling every polygon with a coverage class-specific color, and mapping the color-coded polygons relative to proposed recovery area boundaries (Figures 6-16 and 6-17).

Cautions Regarding Interpretation: *To map vegetation in the entire region of interest, we had to emphasize spatial breadth over local intensity in our sampling design. Thus, our methods are more appropriate for generating inferences about large regions of the study area than, for example, about particular localities. To provide some context for this comment, consider that scenes P41R28 and P41R29 are segmented into more than 1.6 million polygons and cover more than six million hectares. Approximately 10,000 training observations were used to classify these polygons to vegetation type. Although this is a large number of training plots as mapping efforts go, the polygons in which they are placed are a small percentage of the total area. Some error is present in the maps and the estimates derived from the maps.*

The map construction process produced two maps: one showing the predicted forest canopy and nonforest layers, and the second showing predicted forest understory and nonforest layers. The estimated overall map accuracy for the forest canopy and nonforest layer was 68.4% north of the edge-match boundary and 76.7% south of this line. The estimated overall map accuracy for the forest understory and nonforest layer map was 72.3% north of the edge-match boundary and 79.0% south of this line. Coefficients of determination

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(*R*-squared) for the regression models predicting coverage of the primary berry, secondary berry and nut food-plant groups over both scenes ranged from 0.46 to 0.78 and averaged 0.58. A complete evaluation of accuracy for all vegetation type classifications and the bear food-plant coverage estimates is presented in “Results.”

ACKNOWLEDGEMENTS

This “Acknowledgements” section is reproduced verbatim from Hogg, Weaver, Craighead et al. (1999) with the permission of the authors:

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SUMMARY OF RESULTS PERTINENT TO THE FEIS

Important Grizzly Bear Food Producing Habitat:

Landsat Thematic Mapper satellite imagery and botanical survey have been used to develop all-purpose vegetation maps for the Salmon-Selway region of central Idaho (Hogg, Weaver, Craighead et al. 1999). These authors then used these maps and plant species lists from the botanical surveys to estimate the abundance and spatial distribution of food-plant groups important to bears. The USFWS used the text, Tables 6-22, 6-23 and 6-24, and Figures 6-15, 6-16 and 6-17 from that report to produce the following summary statistics and comments regarding important food producing habitats for grizzly bears. The two Landsat scenes used in the CWWI analysis are referred to here as the North and South Scenes (see Figure 6-15). The edge-match boundary between the two scenes lies just south of the Salmon River. The CWWI analyzed several areas within the Bitterroot Ecosystem, including the recovery zone boundaries for Alternatives 1, 2, and 4. Since the Alternative 4 recovery zone boundary roughly approximates the Final EIS Primary Analysis Area (PAA) boundary, the results from analysis of alternatives will be presented here to maintain consistency with other data presented for the PAA in Chapter 3 of the Final EIS. Summaries for Alternative 4 can also be substituted for the experimental area of Alternative 1 and 1A because the boundaries are similar. Alternative 4 and Alternative 4A have the same recovery zone boundaries.

In our summary comments, we have focused on results from the CWWI report related to whitebark pine nuts and several berry producing shrubs because these species provide a major contribution to annual energy demands for bears (Interagency Grizzly Bear Committee 1987). Major berry producing species (referred to as “primary berry species” in the CWWI report) considered included species of huckleberry (*Vaccinium*), serviceberry, cherry, elderberry, buffaloberry, and mountain ash. Secondary berry species included other species producing berries eaten by grizzly bears (Hogg, Weaver, and Craighead et al. 1999).

Whitebark pine nuts are most abundant in the vegetation complex labeled mixed whitebark pine forest (Table 6-22). The estimated total area covered by this complex is 1180 square miles, with 222 square miles in the north scene and 959 square miles in the south scene. Estimated areas of mixed whitebark pine forest within the boundary of each alternative were: 401 square miles in Alternative 1, 101 square miles in Alternative 2, and 1106 square miles in Alternative 4. The authors of the CWWI report built predictive models for the areal coverage of white bark pine tree canopies (Hogg, Weaver, and Craighead et al. 1999). Total areas predicted by this model to be covered by whitebark pine canopies within each alternative were; 63 square miles in Alternative 1, 22 square miles in Alternative 2, and 171 square miles in Alternative 4.

Huckleberry species (*Vaccinium sp.*) are expected to be the dominant berries consumed by grizzly bears in the Bitterroot Ecosystem, but other prominent berry producing species exist such as buffaloberry, serviceberry, mountain ash, and cherry. These major berry species had high coverages in the non-forest vegetation complex labeled mesic shrublands (Table 6-22 and Figure 6-15) and in the understory of certain timber types (Table 6-23). The CWWI classifications of forested areas resulted in maps of both the forest cover type and the understory vegetation complex. We limit the following summary comments regarding the estimated amount of forest land belonging to a given understory complex to those understory vegetation complexes expected to have the highest coverages of huckleberry species other than grouse whortleberry (i.e., understory vegetation codes 40 and 60 in Table 6-23). We will refer to these two understory complexes as timber/huckleberry vegetation types. Total area covered by mesic shrublands was predicted to be 1733 square miles, with 1005 square miles in the north scene and 728 square miles in the south scene. Area of

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mesic shrublands within the boundary of each alternative was predicted to be 235 square miles in Alternative 1, 587 square miles in Alternative 2, and 1147 square miles in Alternative 4. Total area covered by timber/huckleberry vegetation types was predicted to be 5568 square miles, with 2943 square miles in the north scene and 2624 square miles in the south scene. Area of timber/huckleberry vegetation types within the boundary of each alternative was predicted to be 1777 square miles in Alternative 1, 1305 square miles in Alternative 2, and 4480 square miles in Alternative 4. Major berry species occur in significant amounts in several other non-forest and forest-understory vegetation complexes, although coverage of huckleberry species (*Vaccinium sp.*) other than grouse whortleberry is probably lower. The preceding estimates of area covered by vegetation complexes supporting major berries are therefore likely conservative. Furthermore, these area totals emphasized vegetation complexes expected to support relatively high densities of huckleberry species other than grouse whortleberry. Grouse whortleberry can in some years produce a significant crop of berries, but typically is less productive than other species of huckleberry. Grouse whortleberry is often associated with habitats that are drier or cooler, which are more commonly represented in the southern portions of the BE particularly south of the Salmon River .

In addition to whitebark pine (above), the authors of the CWWI report built predictive models for the collective areal coverage of plant species assigned to two other grizzly bear food-plant groups: primary and secondary berries (Hogg, Weaver, and Craighead et al. 1999). Huckleberry, buffaloberry, serviceberry, mountain ash, and cherry were classified as primary berry species (Hogg, Weaver, and Craighead et al. 1999). Numerous other plant species such as kinnikinnick, currant, gooseberry, and raspberry also produce a berry crop that is available to bears. All other such berry producing species were classified as secondary berry species. Total coverage of primary berries within each alternative was predicted to be 724 square miles in Alternative 1, 718 square miles in Alternative 2, and 2059 square miles in Alternative 4. Total coverage of secondary berries within each alternative was predicted to be 193 square miles in Alternative 1, 268 square miles in Alternative 2, and 742 square miles in Alternative 4.

In summary, results of Hogg, Weaver, and Craighead et al. (1999) indicate bear foods in the form of primary and secondary berries are present in biologically significant amounts in both the northern and southern portions of the ecosystem, but generally decline in abundance moving from north to south through the Bitterroot Ecosystem (Table 6-24, Figure 6-16, Figure 6-17). We suspect that this north-south decline in abundance is most marked for species of huckleberry other than grouse whortleberry. However, coverage for this sub-group of primary berry species (excluding grouse whortleberry) was not separately estimated by Hogg, Weaver, and Craighead et al. (1999). Grouse whortleberry could potentially provide a significant seasonal food source in some years. Particularly significant berry distribution occurs north of the Selway-Bitterroot Wilderness area in the North Fork of the Clearwater River drainage and throughout much of the Lochsa and Selway River drainages (Figure 6-16, Figure 6-17). Whitebark pine and associated nut crops tend to follow the opposite pattern with greater abundance and distribution south of the Salmon River and a general decline through the northern portions of the Bitterroot Ecosystem (Figure 6-15).

Table 6-22. Estimated area (hectares and percent of region) of each mapped non-forest, forest canopy and forest understory vegetation complex within various boundaries relevant to the proposed reintroduction of grizzly bears to the Salmon-Selway ecosystem. (Modified from Hoge, Weaver, Craighead et al. [1999], similar data from other sub-regions in the Salmon-Selway ecosystem that are included in Hoge, Weaver, Craighead et al. [1999], but are not defined by an alternative in this FEIS, were omitted from this table.)

	North of		South of		Alternative 1		Alternative 2		Alternative 4	
	edge-match boundary ¹		edge-match boundary ¹							
	Hectares	(%)	Hectares	(%)	Hectares	(%)	Hectares	(%)	Hectares	(%)
Vegetation complexes										
Non-forest										
3100 Xeric grasslands	148,871	(4.8)	305,415	(9.2)	34,489	(2.3)	6,681	(0.5)	98,002	(2.1)
3180 Mesic grasslands/subalpine meadows	110,961	(3.6)	53,725	(1.6)	48,942	(3.2)	59,207	(4.5)	145,510	(3.1)
3200 Mesic shrublands	260,388	(8.4)	188,596	(5.7)	60,896	(4.0)	152,079	(11.4)	297,201	(6.2)
3300 Xeric shrublands	.	.	353,656	(10.7)	77,193	(5.1)	0	(0.0)	244,031	(5.1)
3310 Non-sage xeric shrublands	9,686	(0.3)	.	.	2,636	(0.2)	2,357	(0.2)	6,367	(0.1)
3350 Sage shrublands	32,457	(1.0)	.	.	1,134	(0.1)	791	(0.1)	3,949	(0.1)
3400 Shrub-herbaceous dominated burn	5,858	(0.2)	71,059	(2.2)	25,804	(1.7)	4,464	(0.3)	79,246	(1.7)
6200 Herbaceous riparian	6,871	(0.2)	25,539	(0.8)	3,698	(0.2)	1,522	(0.1)	23,086	(0.5)
7300 Rock dominated	96,753	(3.1)	238,901	(7.2)	122,104	(8.0)	75,603	(5.7)	313,541	(6.6)
Subtotal	671,764	(21.6)	1,239,892	(37.5)	376,896	(24.8)	302,704	(22.8)	1,211,551	(25.4)
Forest canopy										
4203 Lodgepole pine dominated forest	404,626	(15.6)	477,534	(14.4)	215,399	(14.2)	170,404	(12.8)	757,664	(15.9)
4206 Ponderosa pine dominated forest	90,905	(2.9)	166,975	(5.0)	22,117	(1.5)	18,376	(1.4)	108,042	(2.3)
4212 Douglas fir dominated forest	486,958	(15.7)	547,197	(16.5)	334,404	(22.0)	156,196	(11.8)	826,725	(17.3)
4230 D. fir-ponderosa pine dominated forest	.	.	95,306	(2.9)	15,259	(1.0)	0	(0.0)	76,806	(1.6)
4260 Mixed whitebark pine forest	57,433	(1.8)	248,447	(7.5)	103,983	(6.8)	26,263	(2.0)	286,657	(6.0)
4270 Mixed subalpine fir forest	499,243	(16.1)	227,942	(6.9)	278,598	(18.3)	246,528	(18.5)	619,263	(13.0)
4280 Mesic forest	736,028	(23.7)	212,688	(6.4)	144,451	(9.5)	389,394	(29.3)	889,931	(17.0)
4410 Conifer regeneration dominated burn	17,868	(0.6)	22,716	(0.7)	19,543	(1.3)	11,597	(0.9)	39,424	(0.8)
Subtotal	2,373,062	(76.4)	1,998,505	(60.4)	1,133,754	(74.6)	1,018,757	(76.7)	3,524,512	(73.9)
Forest understory²										
10	597,779	(19.2)	.	.	127,042	(8.4)	140,114	(10.5)	292,575	(6.1)
20	277,238	(8.9)	.	.	33,681	(2.2)	158,575	(11.9)	248,302	(5.2)
30	735,358	(23.7)	.	.	171,782	(11.3)	381,948	(28.7)	665,801	(14.0)
40	762,686	(24.5)	.	.	246,711	(16.2)	338,115	(25.4)	552,304	(11.6)
50	.	.	640,565	(19.4)	158,023	(10.4)	5	(0.0)	488,779	(10.2)
60	.	.	679,988	(20.5)	213,824	(14.1)	0	(0.0)	608,630	(12.8)
70	.	.	157,100	(4.7)	51,427	(3.4)	0	(0.0)	153,654	(3.2)
80	.	.	520,852	(15.7)	131,265	(8.6)	0	(0.0)	514,467	(10.8)
Subtotal	2,373,062	(76.4)	1,998,505	(60.4)	1,133,754	(74.6)	1,018,757	(76.7)	3,524,512	(73.9)
Other ³	63,030	(2.0)	70,957	(2.1)	8,438	(0.6)	7,546	(0.6)	33,819	(0.7)
Total	3,107,856	(100.0)	3,309,354	(100.0)	1,519,089	(100.0)	1,329,007	(100.0)	4,789,883	(100.0)

¹ A missing value (-) indicates that the corresponding vegetation complex was not mapped for this region.

² See Table 6-23 for an ecological characterization of understory complexes.

³ urban, agriculture, water, snow, cloud, and cloud shadow

Table 6-23. Ecological characterization and numeric code for the eight forest understory vegetation complexes mapped in P41R28 and P41R29 (Modified from Hogg, Weaver, Craighead et al. [1999]).

TM scene	Understory vegetation complex code	Temperature class	Moisture class	Understory indicator species	Trees present ¹
P41R28	10	warm	dry to moist	bunchgrass, ninebark, mountain snowberry, pinegrass, blue huckleberry	ponderosa pine, douglas fir
	20	warm	wet	queencup beadlily, wild ginger	western redcedar, grand fir
	30	warm to cool	moist to wet	queencup beadlily, twinflower, twisted stalk	grand fir, subalpine fir
	40	warm to cold	dry to moist	huckleberry, grouse whortleberry, beargrass, false huckleberry, bluejoint, smooth woodrush	grand fir, lodgepole pine, mountain hemlock, subalpine fir, whitebark pine
P41R29	50	hot to warm	dry to moist	bunchgrass, ninebark, mountain snowberry, pinegrass, elk sedge, white spirea	ponderosa pine, douglas fir
	60	warm to cool	dry to moist	queencup beadlily, pinegrass, blue huckleberry, false huckleberry	douglas fir, grand fir, lodgepole pine, subalpine fir
	70	cool to cold	moist	grouse whortleberry, beargrass, bluejoint, smooth woodrush	lodgepole pine, subalpine fir
	80	cold	dry	grouse whortleberry, elk sedge	lodgepole pine, subalpine fir, whitebark pine

¹ Characteristic species existing in the canopy or regenerating in the understory.

Appendix 21D - Food-Producing Habitats in the BE for Grizzly Bears

Table 6-24. Total area (thousands of hectares and percent of region) predicted by regression analysis to be covered by species belonging to each of three grizzly bear food-plant groups, and predicted distribution of area within each proposed recovery boundary across the coverage value classes mapped in Figures 6-16 and 6-17. (Modified from Hogg, Weaver, Craighead et al. [1999]; similar data from other sub-regions in the Salmon-Selway ecosystem that are included in Hogg, Weaver, Craighead et al. [1999], but are not defined by an alternative in this FEIS, were omitted from this table.)

FOOD GROUP	COVERAGE CLASS	ALTERNATIVE 1			ALTERNATIVE 2			ALTERNATIVE 4		
		Estimated area in coverage class ¹		Estimated area covered by food group ² (thousands of hectares)	Estimated area in coverage class ¹		Estimated area covered by food group ² (thousands of hectares)	Estimated area in coverage class ¹		Estimated area covered by food group ² (thousands of hectares)
		Thousands of hectares	(%)		Thousands of hectares	(%)		Thousands of hectares	(%)	
Primary berries										
	0-1% ³	308.0	(20)		156.3	(12)		903.1	(19)	
	1-5%	276.8	(18)		241.6	(18)		1,084.6	(23)	
	5-15%	495.5	(33)		569.1	(43)		1,622.5	(34)	
	15-25%	139.9	(9)		43.8	(3)		407.1	(8)	
	25-50%	298.4	(20)		318.2	(24)		751.0	(16)	
	50-100%	0.5	(0)		0.0	(0)		1.6	(0)	
	All classes	1,519.1	(100)	187.6	1,329.0	(100)	186.0	4,769.9	(100)	533.2
Secondary berries										
	0-1% ³	747.5	(49)		522.3	(39)		2,120.8	(44)	
	1-5%	362.7	(24)		202.9	(15)		1,091.8	(23)	
	5-15%	375.9	(25)		497.4	(38)		1,367.9	(29)	
	15-25%	28.9	(2)		83.7	(6)		148.0	(3)	
	25-50%	4.0	(0)		22.6	(2)		41.3	(1)	
	50-100%	0.1	(0)		0.1	(0)		0.1	(0)	
	All classes	1,519.1	(100)	50.1	1,329.0	(100)	69.5	4,769.9	(100)	192.2
Nuts										
	0-1% ³	1,279.5	(84)		1,206.4	(91)		4,052.0	(85)	
	1-5%	133.1	(9)		96.1	(7)		426.7	(9)	
	5-15%	85.9	(6)		23.6	(2)		245.5	(5)	
	15-25%	16.5	(1)		2.1	(0)		36.2	(1)	
	25-50%	4.0	(0)		0.7	(0)		9.2	(0)	
	50-100%	0.1	(0)		0.1	(0)		0.3	(0)	
	All classes	1,519.1	(100)	16.4	1,329.0	(100)	5.7	4,769.9	(100)	44.4

¹Calculated as the sum of areas for all polygons in the region of interest predicted to have a food group coverage within the range specified for the coverage class.

²Calculated as the product of polygon area and predicted coverage summed over all polygons in the region of interest.

³This class includes regions mapped white and blue in Figures 6-16 and 6-17.

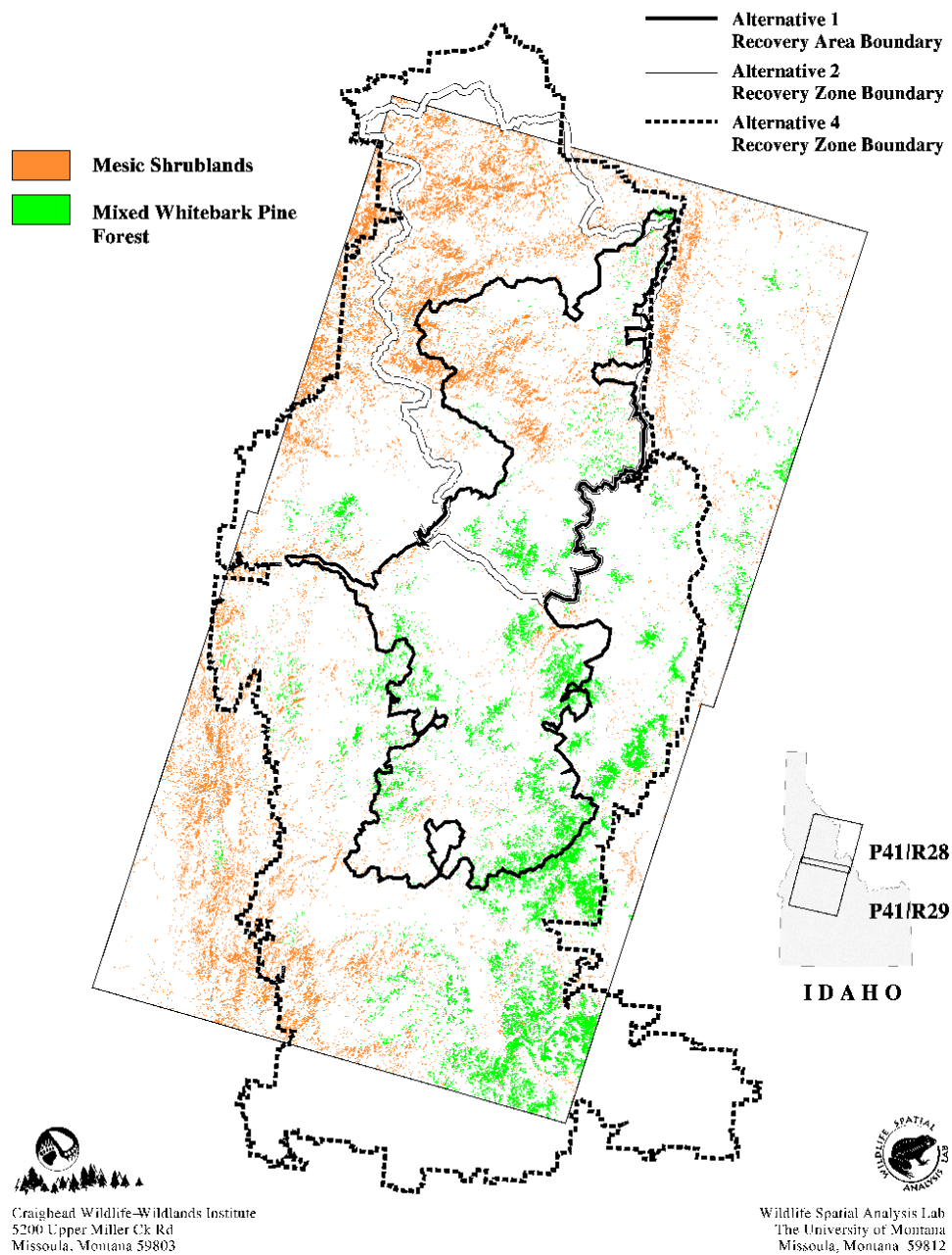
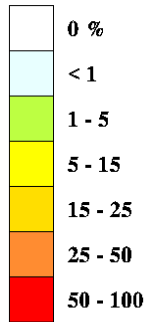


Figure 6-15. Estimated distributions of Mixed Whitebark Pine Forest and Mesic Shrublands vegetation complexes in the Salmon-Selway Ecosystem.

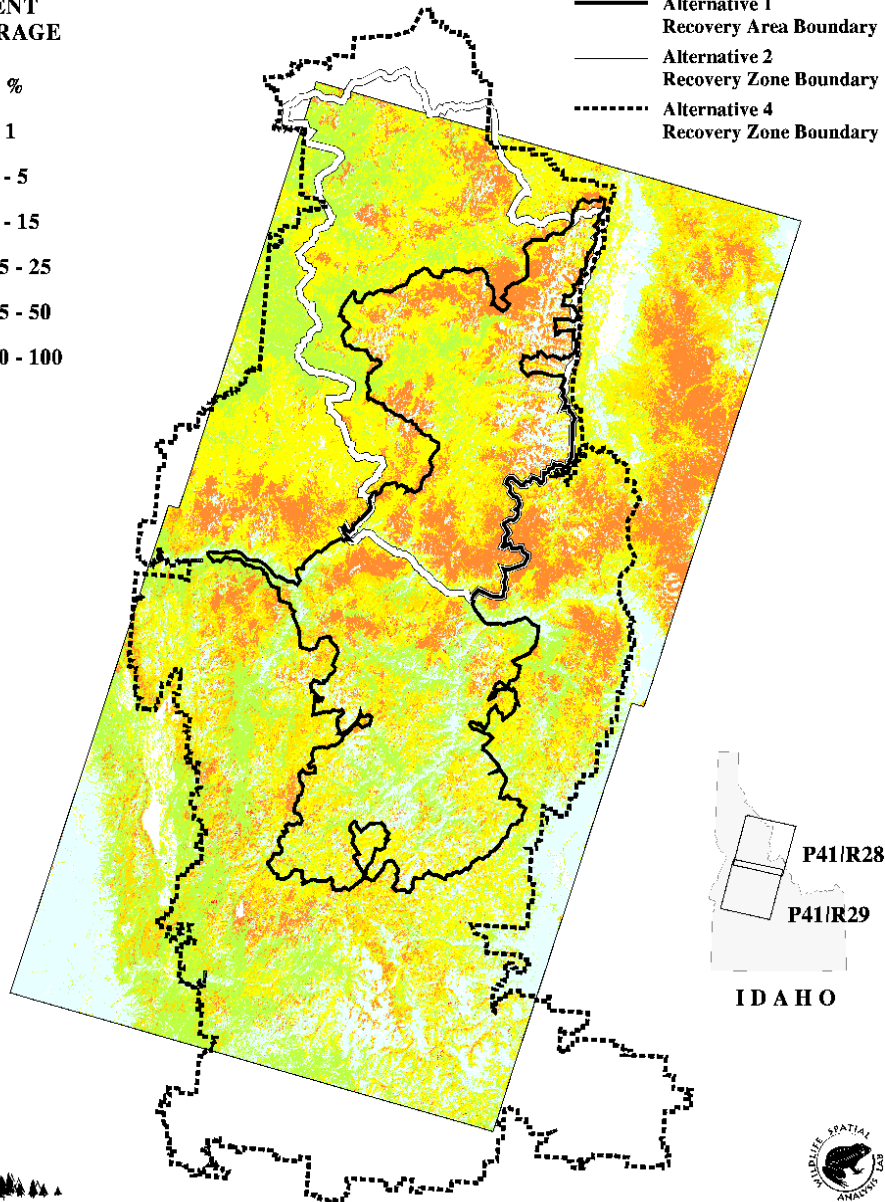
Appendix 21D - Food-Producing Habitats in the BE for Grizzly Bears

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**PERCENT
COVERAGE**



- Alternative 1
Recovery Area Boundary
- Alternative 2
Recovery Zone Boundary
- Alternative 4
Recovery Zone Boundary



Craighead Wildlife-Wildlands Institute
5200 Upper Miller Ck Rd
Missoula, Montana 59803

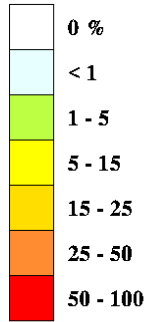


Wildlife Spatial Analysis Lab
The University of Montana
Missoula, Montana 59812

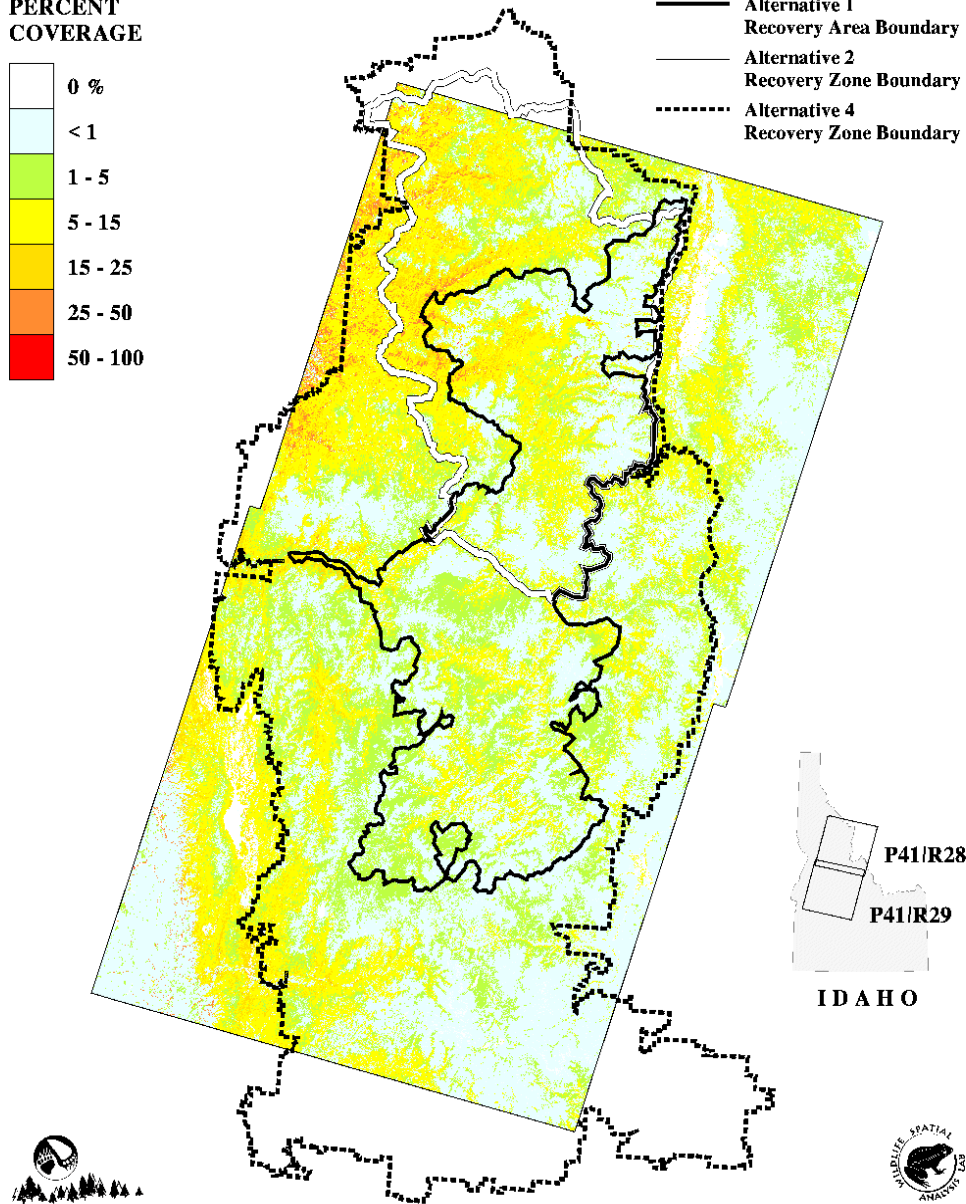
Figure 6-16. For the Salmon-Selway Ecosystem, estimated percent coverage of plants that produce berries reported to be of primary importance to grizzly bears in other ecosystems.

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**PERCENT
COVERAGE**



- Alternative 1
Recovery Area Boundary
- Alternative 2
Recovery Zone Boundary
- Alternative 4
Recovery Zone Boundary



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Figure 6-17. For the Salmon-Selway Ecosystem, estimated percent coverage of plants that produce berries reported to be of secondary importance to grizzly bears in other ecosystems.

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